

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:27:32 ; Search time 44 Seconds
(without alignments)
1431.942 Million cell updates/sec

Title: US-10-663-157-2
Perfect score: 3456
Sequence: 1 MGTPSSSTALASCSRIARR.....SQEASOTLDSVYSHLPDLL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2350	68.0	651	2 JC7705	death receptor-6 -
2	343.5	9.9	461	1 A5356	tumor necrosis fac
3	275.5	8.0	459	2 I49854	Gene murine tumor
4	273.5	7.9	474	2 B38534	tumor necrosis fac
5	236.5	6.8	416	1 JN0006	nerve growth facto
6	235.5	6.8	255	2 I38426	lymphocyte activat
7	233	6.7	305	2 A46476	B cell-associated
8	228.5	6.6	435	2 I34182	tumor necrosis fac
9	218.5	6.3	326	1 GQZML	T2 protein - myxom
10	211.5	6.1	325	2 B3592	T2 protein - rabbi
11	211.5	6.1	425	1 A26431	nerve growth facto
12	210.5	6.1	427	1 GQHUN	nerve growth facto
13	206.5	6.0	348	2 T28623	hypothetical prote
14	206.5	6.0	349	2 D36858	gene G4R protein -
15	205	5.9	595	2 A42086	CD30 antigen precu
16	204.5	5.9	349	2 D72175	G2R protein - vari
17	200	5.8	277	2 A60771	B-cell activation
18	193	5.6	461	2 J24302	tumor necrosis fac
19	191.5	5.5	2824	2 T22759	hypothetical prote
20	187.5	5.4	493	2 JC5486	membrane glycoprot
21	186.5	5.4	461	1 GQRTT1	tumor necrosis fac
22	180.5	5.2	256	2 B32393	T-cell antigen 4-1
23	170	4.9	454	1 GQMTT1	tumor necrosis fac
24	154	4.5	277	2 I37552	OX40 homolog - hum
25	148	4.3	271	2 T2783	OX40 antigen precu
26	145.5	4.2	455	1 GQHUT1	tumor necrosis fac
27	142.5	4.1	1193	2 A44018	laminin B2t chain
28	138	4.0	1827	2 T34288	hypothetical prote
29	136.5	3.9	1205	2 T27053	hypothetical prote

30	136.5	3.9	1372	2 T25933	hypothetical prote
31	136	3.9	272	2 I49700	gene ox40 protein
32	135.5	3.9	5376	2 T42215	zonadhesin - mouse
33	132.5	3.8	1252	2 S35016	oocyst wall protei
34	129.5	3.7	3570	2 T45025	mucin MUC5B, trach
35	129	3.7	1459	2 T30196	kinesin motor prot
36	128.5	3.7	634	2 T00388	hypothetical prote
37	128.5	3.7	987	2 I48652	mouse developmenta
38	128.5	3.7	1032	2 T34433	hypothetical prote
39	128.5	3.7	2232	2 T34434	hypothetical recept
40	127.5	3.7	987	2 I48953	eph-related recept
41	126	3.6	1440	2 T27842	lin-15B protein -
42	125.5	3.6	1379	1 S01254	hepatocyte growth
43	123.5	3.6	557	2 A48434	variant-specific s
44	123.5	3.6	1367	1 S48478	glucan 1,4-alpha-g
45	123	3.6	2183	2 T42764	coagulation factor

ALIGNMENTS

RESULT 1

JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C:Accession: JC7705
R:Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705, MUID:21308433, PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.
C:Genetics:
A:Gene: dr-6
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 68.0%; Score 2350; DB 2; Length 651;
Best Local Similarity 70.6%; Pred. No. 5.8e-148;
Matches 459; Conservative 47; Mismatches 102; Indels 46; Gaps 10;

QY	23	ATWIASLLLLGLFSLTTTAQ-----	EOKASNL-IGTVRHVDRTAQVLTCDKCPAGTVYS	77
DB	3	AAVLAALVLLVFLGTLADAPQLK	TSEQNAVSLSAGKYLLDRATNQELICDKCPAGTVYS	62
QY	78	EHCNTSLRVCSGCPVGTFTRHENGIEK	CHDCSQCPCEWPMIEKLPCAALTRECTCPGM	137
DB	63	KHCTKSTLRBCSPCPDGTFTKHENGIER	CHCPKRPCELPMEIKTHCTALTRECTCLSGT	122
QY	138	FOSNATCAHTVCPVGWVRKKGTTETED	VRQCQARGTFSDVPSSVMKCAVTDCLSQL	197
DB	123	FQINDTCVPTVCPVGWVRKKGTTETED	VRCKPCLRGTFSDVPSSVMKCTYTDGFGKM	182
QY	196	VWIKGTKETNVG-----GTLP--	SFSSSTSPSGCTAIPRPEHMETHEVPSSTYVPKGMN	252
DB	183	VVVKPGTKESDNCVKSPLNTSLTSSDAQD	-----ETYEAPPTAYLPKGLN	232
QY	253	STESNNSASVPKVLISSIQEGTVDPNT	SSARGKEDVNKTLPLNVVHHQGGPHRHILKL	312
DB	233	SSVFDLSSSPAPRVNSGTAEPTVDYNDT	SANGTVGAPGSLSAGTAGQAQSVYRKHKTSQA	292
QY	313	L-----PSMEATGCKSSTPIKGP	KGRQNLHKHFDINEHLPWVILFLVLLVIVVICS	369

A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g803043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
C;Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product:tumor necrosis factor receptor type 2 #status predicted <MAT>
F:48-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 7.9%; Score 273.5; DB 2; Length 474;
Best Local Similarity 25.0%; Pred. No. 1.5e-10;
Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;

Qy 65 LTCDKCPAGYVSEHCNTSLRVCSQCPVGTFTTHENGIEKCHDCSPCPWPMIEKLPDA 124
Db 53 MCCA KCPGGVGVKHFCKNKTSDTVACDCEASMYTVQMNQFRTCLSCSSCTDQVEIRACT 112
Qy 125 ALTDRECTCPGPFQSNAT-----CAPHTVCPGVGVGRKKGTETEDVRCKQCARGTF 177
Db 113 KQNRVCAACAGRYCALKTHSGRCQVRLSKCGFGGVASSRAPNGVNLCKACAPGTF 172
Qy 178 DVPSSVMKCKAYTDCLSQNLVVIKPGTKETDINVCGTLPFSFSSSTSPSPGTAIFRPRHME 237
Db 173 DTTSSTDVCRPHRIC---SILAIPGNASTDAVCA-----PESPT 208
Qy 238 THEVPSSTYV----PKGMNTESSNSASVPKVLSSIQEGTVPONTSSARGKEDVUNKTLP 293
Db 209 LSAIPRTLYSQPEPTRSQPLDQPGSPQPSILTSL--GSTPIEQSTKG---GISLP 262
Qy 294 -----NLQVYN-----HQQGP-----HRLIK 311
Db 263 IGLIVGTVSLGLMLGLVNCILVQRKKPSCQLORDAKVPHVDEKSDQAVGLEQOHLT 322
Qy 312 LLFSMEATGEGKST--PIKPKRGHPR 337
Db 323 TAPSSSSSSLESSASAGDRRAPGQHQP 350

RESULT 5
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reineuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor in A;Reference number: JN0006; MUID:90166579; PMID:2560385
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatale-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma C;Comment: The cysteine-rich region of the extracellular domain may form part or all of C;Comment: This protein is thought to form a high-affinity receptor when it associates C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:58-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>

F:141-181/Domain: NGF receptor repeat homology <NG4>

F:189-237/Region: serine/threonine-rich

F:240-261/Domain: transmembrane #status predicted <MEM>

F:262-416/Domain: intracellular #status predicted <INT>

F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 236.5; DB 1; Length 416;

Best Local Similarity 23.2%; Pred. No. 3.7e-08;

Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;

QY 67 CDKCPAGTVVSEHCNTSLRYCSSC-PVGTPTREHNGIEKCHDCSQCPMPMIEKLPCAA 125

Db 36 KCACNLGGVQPC-GVNQTVCEPCLDSVTYSDVATSECKPCTQ-CVGLHSMSPCVE 93

QY 126 LTDBECTPPGMFQS--NATCAPHTVCPVGVGRKKTETEDVRCKQCARGTSDVPSSV 193

Db 94 SDDAVCRAYGYFQDEJSGSKESICEVGFGLMFPQRDSQDTCCECPGTFSEANFV 153

QY 184 MKCKAYTDCLSQNLVVIKPGTKETDNVCGTL-----PSFSSSTSPSPGTAFPRPEH 235

Db 154 DPLPCTIC-BENEMVKECTATDAECRLHPRWTHTFSLAGSDSPETIRDPNTEG 212

QY 236 MATHVPSSTVYKGMSTENSSAS-----VRPKVLSIOEGTVDPDNTSSARGKEDVNKT 291

Db 213 MATTLADIIVTVMGSSQPVWGRGTADNLIPYCSILAAVVGVLVAYIAFRWNSCKQNK 272

QY 292 LPNLQVNHQGGPHRHILKLLPSMEATGGKSTPIKPKRGHPRONLKHFDINEHLP 351

Db 273 GANRPVNTSPSE-----GEX-----LHSDSGI----- 236

QY 352 WMIVLFLVLVVIWVCSIRKSRSLKGRQDPESAIVEK--AGLKKSMTPTONREKWIY 409

Db 297 -----SVDQSLLHQDPFNQSTQGPAPKDGSLYASLPSPKQEE----- 335

QY 410 YNCHGIDILKLVAAQVGSQKDIYQFLCNASREVAFNGY-----TADHERAYA 461

Db 336 -----VEKLSSSAEETWRQL-----AGELGYKEDLIDCFTEESPARA 374

QY 462 ALQHWITRGPEASLAQILSALRQHRNRNDVVEKI 494

Db 375 LLADWSAK-ETATLDALLVALRKIQRGDIAESL 406

RESULT 6

I38426

Lymphocyte activation-induced receptor ILA precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000

C:Accession: I38426; J70752

R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R

Sur, J. Immunol. 24, 2219-2227, 1994

A:Title: Molecular and biological characterization of human 4-1BB and its ligand.

A:Reference number: I38426; MUID:94374434; PMID:8088337

A:Accession: I38426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-255 <RES>

A:Cross-references: EMBL:U03397; NID:9571320; PIDN:AAA53133.1; PID:9571321

R:Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne

A:Reference number: J70752; MUID:94085794; PMID:8262389

A:Accession: J70752

A:Molecule type: mRNA

A:Residues: 1-106, R', 108-255 <SCH>

C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-neoc

C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F:187-213/Domain: transmembrane #status predicted <TM>

F:136,149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted

F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 6.8%; Score 235.5; DB 2; Length 255;

Best Local Similarity 30.4%; Pred. No. 2.3e-08;

Matches 63; Conservative 24; Mismatches 77; Indels 43; Gaps 8;

QY 25 MIAGSLLGLGLSTTTAQPEQKASNLIGTYRHVDRATQVLTCDKCPAGTVVSEHCNTS 84

Db 8 IVATLLLVNLFERTSLQD-----PCNCPAGTF-----CDNR 41

QY 85 LRVCSGCVPTGFTREHNGIEKCHDCSQCPMPMIEKLPAAALTDRECTPPGMFQSNATC 144

Db 42 NQICSPCPNFS-SAGGORTCDICRQ--CKGVTRTRKCSSTNAECDCCTGPFHCLGAGC 99

QY 145 AP-HTVCPVGVGRKKTETEDVRCKQCARGTSDVPSSVMKCKAYTDCLSQNLVVIKPG 203

Db 100 SMCEQDCQGGQELTKG-----CKCCFGTFNDQKRGI--CRPWTNCSLDGKSLVNG 150

QY 204 TKETDNVCGTLPS-----FSSSTSPSP 225

Db 151 TKERDVVCGSPADLSPGASSVTTPAP 177

RESULT 7

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C:Accession: A46476; A46515

R:Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A:Reference number: A46476; MUID:92105763; PMID:1370315

A:Accession: A46476

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305 <TOR>

A:Cross-references: GB:M83312; NID:91553058

A:Note: sequence extracted from NCI backbone (NCBIN:75206, NCBI:75207)

A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,

J. Immunol. 149, 3921-3926, 1992

A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A:Reference number: A46515; MUID:93094586; PMID:1281194

A:Accession: A46515

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-287, 'LV', <GRI>

A:Cross-references: GB:M83312; NID:91553058; PIDN:AA08705.1; PID:91553059; GB:M94126; N

A:Experimental source: BALB/c, liver

A:Note: sequence extracted from NCI backbone (NCBI:120357)

C:Comment: For an alternative splice form, see PIR:A46515.

C:Comment: For an alternative splice form, see PIR:A46476.

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: alternative splicing; transmembrane protein

F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 6.7%; Score 233; DB 2; Length 305;

Best Local Similarity 34.9%; Pred. No. 4.2e-08;

Matches 53; Conservative 21; Mismatches 70; Indels 8; Gaps 4;

QY 67 CDKCPAGTVVSEHCNTSLRVCSGCVPTGFTREHNGIEKCHD---CSQCPMPMIEKLPC 123

Db 38 CULQPGRLTSHCTALKECTQCHPCDSGEFAQWNRREIRCHQHRHC-EPNQLRVKK-EG 95

QY 124 AALTDRECTPPGMFQSN---ATCAPHTVCPVGVGRKKTETEDVRCKQCARGTSDVP 180

Db 96 TAESDVTCTCKEGQCTCKDCEACAQHTPCIPGFGVEMEMATETDITDVTCHPCPVGFSSQS 155

QY 181 SSMKCKAYTDCLSQNLVVIKPGTKETDNVCG 212

Db 156 SLFEKCYPTWSCEDKNLEVLQGRGTSQTNVIG 187

RESULT 8

I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequences
A:Reference number: I54182; MUID:93252381; PMID:8486360
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.6%; Score 228.5; DB 2; Length 435;
Best Local Similarity 30.9%; Pred. No. 1.3e-07;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSFCVGTFTFRHENGIEKHCDCQPC-PWPMTIEKL-P 122
DB 57 ICCSRCPGTGYVSXKSRIRDTVCATCAENSYNEHWNLYLTICQLC-RPCDPVWGLEETAP 115
QY 123 CAALTDRECTCPGQFQSNATCAHTV-----CPVGVGRKKTEYE----- 164
DB 116 CTSKSKTKCQCPQGMF-----CAAWALECTHCELLSDCP-----PGTEAELKDEVGKG 163
QY 165 DVRCQKQARGTSDVPSSVMKCKAYTDCLSQNLVVKGTETONVCGT----LPSFSS 220
DB 164 NNHCVPCKAGHQNTSSPSARCPHTRCENQGLVEAEGTAQSDITCKNPLELPPEMSG 223
QY 221 T 221
DB 224 T 224

RESULT 9

QVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 15-Sep-2003
C:Accession: A40566
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor
A:Reference number: A40566; MUID:91335768; PMID:1651597
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 218.5; DB 1; Length 326;
Best Local Similarity 36.8%; Pred. No. 4.2e-07;
Matches 50; Conservative 10; Mismatches 69; Indels 7; Gaps 2;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSFCVGTFTFRHENGIEKHCDCQPC-PWPMTIEKLPCA 124
DB 38 LCCTSCPEGSYASRLCGPSDTCVSPCKNETFTASTNHAPACVSCRGCTGHLSESQSCD 97
QY 125 ALTDRECTCPGMF-----QSNATCAPHTVCPVGVGRKKGTETEDVRCKQARGTFSD 178

DB 98 KTRDRVCDCCAGNVCLLKGCGCRICAPKTKCAGYGV-SGHTRTGDVLTCKCPRTYSD 156
QY 179 VPSSVMKCKAYTDCLS 194
DB 157 AVSSTETCTSSFNYS 172

RESULT 10

B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103; PMID:2820128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 6.1%; Score 211.5; DB 2; Length 325;
Best Local Similarity 36.7%; Pred. No. 1.2e-06;
Matches 47; Conservative 7; Mismatches 67; Indels 7; Gaps 2;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVCSFCVGTFTFRHENGIEKHCDCQPC-PWPMTIEKLPCA 124
DB 38 LCCASCHPGFYASRLCGPSDTCVSPCKNETFTASTNHAPACVSCRGCTGHLSESQPCD 97
QY 125 ALTDRECTCPGMF-----QSNATCAPHTVCPVGVGRKKGTETEDVRCKQARGTFSD 178
DB 98 RTHDRVCMNSTGNYCLLKQNGCRICAPKTKCAGYGV-SGHTRAGTLCCKCPRTYSD 156
QY 179 VPSSVMKC 186
DB 157 SLSPTERC 164

RESULT 11

A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1997
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859; PMID:3027580
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:g56756
R:Metzsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinol
A:Reference number: PH1229; MUID:93077038; PMID:1446821
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Genetics: 20/3
A:introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Domain: NGF receptor repeat homology <NG5>
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 211.5; DB 1; Length 425;
Best Local Similarity 22.9%; Pred. No. 1.7e-06;
Matches 119; Conservative 59; Mismatches 196; Indels 145; Gaps 25;

QY 12 ASCSRIARATMIAGSLLGLFSTTTAQPEQKASNLIGTYRHVRATQVLTCDKCP 71
DB 6 AACSAIDL-----RLLLLLILGVSSGGAKETCT--GLYTH-----SGE--CCRACN 49

QY 72 ACTYSEHCNTSLRVCCSPVG-TFTREHNGIEKCHDCSPCPWPMIEKLPALTDRE 130
DB 50 LQEGVAQPC-GANQTVCEPCLDNVTFSDVWSATEPCKPCTE-CLGLQSMSPAPCVADDAV 107

QY 131 CTCPPGMFOSNAT--CAPHTVCPVCGVYRKKGTETEDVRCKOCARGTFSDVPVSMKCKA 188
DB 108 CRCAVGYQDETHGCEACSVCEVSGGLVFCQDKQNTVCECEPGIYSDANHVDFCLP 167

QY 189 YTDCLSNLWLWIKPQKTDNDVCGTLPSFSSSTSPSPGTALFPPEHMETHEVPSSTVYP 248
DB 168 CTVC-EDTERQLRECTPWADABCEBIPG-----RWIPRST-PP 203

QY 249 KGMNNT-ENSSASRPVKLSIQEGTVPDNTSSARGKEDVKNLPLNQLVNVHQGPHR 307
DB 204 EGSDDSTAPSTQPEVFPPE--QDLVSTVADVMVTVMG----- 238

QY 308 HILKLLPSMEATGEGKSSTPIKGRGHRPQNLHFKHFDINELPMVILFLLVLVIVV 367
DB 239 -----SSQPV--VTRG-TTDLN-----IP-VYCSILAAVAVGLV 268

QY 368 CSIR-----KSSRTLKGRQDPSAIVKAGLKKSTPTQNKREKVIYVNCNGHIGILKVA 423
DB 269 AYIAFKRMNSCKQNKQANSRP-----VNQTPPEGEK-LHSDSGISVDSQSUDH 317

QY 424 AQVGSQWK-----DIYQFLCNASREVAAPNGVTADH---ERAY----- 460
DB 318 QQTHQTASGOALKGDGNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSPFHE 377

QY 461 -----AALQHTWITRGEASLAOLISALRQHRNDVVEKI 494
DB 378 ACPVRALLASWGAQ-DSATLDALLAALRIQRADIVESL 415

RESULT 12
GQUHN
Nerve growth factor receptor precursor, low affinity [validated] - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:q189204; PIDN:AAB59544.1; PID:q189205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A;Reference number: A60204; MUID:87085574; PMID:3025363

A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31, 'T', '33-42, 'TT', '45-46, 'TX', '50-51, 'XX', '54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleot
R;Visavajjalala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:q189206; PIDN:AAA36363.1; PID:q189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Domain: NGF receptor repeat homology <NG5>
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Best Local Similarity 22.8%; Pred. No. 2e-06;
Matches 116; Conservative 58; Mismatches 204; Indels 131; Gaps 22;

QY 21 ATATAGSILLGLFSTTTAQPEQKASNLIGTYRHVRATQVLTCDKCPAGTYVSEHC 80
DB 5 ATGRMDGPRLLLLLLGLVSLGKAECAP-TGLYTH-----SGE--CCRACNLGEVQAPC 57

QY 81 TNTSLVCSQC-PVGTFTREHNGIEKCHDCSPCPWPMIEKLPALTDRECTCPGMQ 139
DB 58 -GANQTVCEPCLDSVTFSDVWSATEPCKPCTE-CVGLQSMSPAPCVADDAVCRCAVGYQ 115

QY 140 SNAT--CAPHTVCPVCGVYRKKGTETEDVRCKOCARGTFSDVPVSMKCKAVTDCLSQNL 197
DB 116 DETTGCEACRCEAGSLVFCQDKQNTVCECEPGIYSDANHVDFCLPCTVC-EDTE 174

QY 198 VWIKPQKTDNDV-----GTLPSFSSSTSPSPGTALFPPEHMETHEVPSSTV 247
DB 175 RLQRECTRWADABCEBIPGRWTRSPPEGSSTAPST-----QSPEAPEQDLASTVA 229

QY 248 PKGMNSTENSSASVPPK-----VLSIQEGTVPDNTSSARGKEDVKNLPLN 295
DB 230 --GVVTVMGSSQPVVTRGTTNLPVYCSILAAVAVGLVAYIAFKRMNSCKQNKQANS 287

QY 296 QVNVHQGPHRHILKLLPSMEATGEEK--SSTPIKGRGHRPQNLHFKHFDINELPMV 353
DB 288 RPNVQTFPPE-----GKHLSDSGISVDS-----QSLH---DQPH---- 320

QY 354 IVFLLLVLVIVVVCIRKSSRTLKGRQDPSAIVKAGLKKSTPTQNKREKVIYVNCNG 413

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Db 321 -----TQTASGQALKG-----DGLGYSLPPAKREE----- 346
QY 414 HGIDILKLVAAQVQSQWKDIYQFLCNASERVAFSNGYTAADHERAY-----AALQH 465
Db 347 -----VEKLNGSAGDTWRHL-----AGELGYQPEHIDSFTHREACPVRALLAS 389
QY 466 WTIRGPEASLAQLISALRQHRNDVVEKI 494
Db 390 WATQ-DSATLDAALLARLRIQADLVESL 417

RESULT 13
T28623
Hypothetical protein G2R - variola major virus
C:Species: variola major virus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C:Accession: T28623
R:Massung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 6.0%; Score 206.5; DB 2; Length 348;
Best Local Similarity 34.1%; Pred. No. 2.9e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;

QY 65 LTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTTRHENGIEKCHDCSQCPWPWMIKLPKA 124
Db 41 LCCLSCPPTGYASRLCDSKNTQCTPCGSGFTSRNNHLPACLSGRCNSNQVETRSCN 100

QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGWVRKKGTTETEDVRCKQCARGTFSD 178
Db 101 TTHNRICEPSGYCYLLKSGSCKACVSTQKCGIGYV-SGHTSVGDVICSFGCGFTYSH 159

QY 179 VPSSVMKCK 187
Db 160 TVSSADKCE 168

RESULT 14
D36858
Gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA49137.1; PID:9457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46888
A:Accession: S46888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A:Experimental source: strain India-1967, isolate Ind3

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R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 6.0%; Score 206.5; DB 2; Length 349;
Best Local Similarity 34.1%; Pred. No. 2.9e-06;
Matches 44; Conservative 12; Mismatches 66; Indels 7; Gaps 2;

QY 65 LTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTTRHENGIEKCHDCSQCPWPWMIKLPKA 124
Db 42 LCCLSCPPTGYASRLCDSKNTQCTPCGSGFTSRNNHLPACLSGRCNSNQVETRSCN 101

QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGWVRKKGTTETEDVRCKQCARGTFSD 178
Db 102 TTHNRICEPSGYCYLLKSGSCKACVSTQKCGIGYV-SGHTSVGDVICSFGCGFTYSH 160

QY 179 VPSSVMKCK 187
Db 161 TVSSADKCE 169

RESULT 15
A42086
CD30 antigen precursor - human
N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A42086
R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A:Title: Molecular cloning and expression of a new member of the nerve growth factor re
A:Reference number: A42086; MUID:92154659; PMID:1310894
A:Accession: A42086
A:Molecule type: mRNA
A:Residues: 1-595 <DUR>
A:Cross-references: GB:M83554; NID:9180095; PIDN:AAA51947.1; PID:9180096
A:Experimental source: HUT-102 cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
C:Genetics:
A:Gene: GDB:CD30; DIS166E
A:Cross-references: GDB:I31547; OMIM:153243
A:Map position: lp36-lp36
C:Superfamily: NGF receptor repeat homology
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-383/Domain: extracellular #status predicted <EXT>
F:384-407/Domain: transmembrane #status predicted <TM>
F:408-595/Domain: intracellular #status predicted <CYT>
F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 205; DB 2; Length 595;
Best Local Similarity 20.2%; Pred. No. 7.1e-06;
Matches 131; Conservative 66; Mismatches 250; Indels 200; Gaps 24;

QY 30 LLLLG--FLSTTAAEQEK--ASNLGTGYRH-VDRATGQVLTCDKCPAGTYVSEHCTNTS 84
Db 5 LAALGLLFGALRAFFQDPFFEDTCHGNPSHYDKAVRR--CCYRCFPMGLFFQCPQRP 62

QY 85 LRVCSGCPVGTTRHENGIEKCHDCSQCPWPWMIKLPACALTDRECTCPGMPF----- 138
Db 63 TDCRQCEPYIIDADRCTACTCGRD---DLVETPCAWNSRVCRCRPGMFCSTSAV 119

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QY 139 QNATCAPHTVCPVGVKKGKGTETEDV-----RCQOCARGTF----- 176
Db 120 NSCARCFHSHVCPAGMIVKFGPTAQKNTVCEPASGVSPACASPENCCKEPPSSGTPQAKP 179
QY 177 -----SDVPSSV----- 183
Db 180 TPVSATSSASTMPVRGGTRLAQEAASKLTRAPDSPSVGRPPSSDPGLSPQCPESGSD 239
QY 184 -----MKKAYTDCLSNLVVVKPGTKETDNVCGTLPFSFSSSTSPSGTA- 228
Db 240 CRKQCEPDYLDAGRCIACVSCSRDDLVEKTPCAWNSRRTCECPGMICATSNSCAR 299
QY 229 IFPRPEHMETHEVPSTYVPKGMNSTESNSASVBPVKVLSIOEGTVPDNTSSARGKEDV 288
Db 300 CVFYP-----ICAAETVKPDMAEKDITFEAPPL-----GTQPCNPTPENGAP 345
QY 289 NKTLENLQVNNHQGPVHRRHILKLLPSMEATGGEKSTPIKPKRGHPRONLKHFDINE 348
Db 346 ASTSPQSLVDSQAS-----KTLPI-----PTSAPVALSSTGKP-----VLDAGP 386
QY 349 HLPWMIVLELLVLVIV-----VCSTRKSRTLKKG-----PRQDPSAIVEKAGLKKS 397
Db 387 VLFWVI-----LVLVVVVSSAFLCHRRACRKRIRQKHLCPVQTSQPKLELVDSRPR 441
QY 398 MPTQNRKWIYYCNGHGIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHE 457
Db 442 RSTQURS-----GASVTEPVAERGLMSQPLME-TC-----HS 474
QY 458 RAYAALOHWTIR-----GPEASLAQLISALRQHRNDVVEKIRGLMEDTTQLETDKLAL 511
Db 475 VCAAYLESPLQDASPAGSPSPRDLPEPRVSTHTNNKIEKIYIMKADTVIVGTVKAE 534
QY 512 PMSPSPLSPSPSPNAKLENSALLTVBPSQDKKKGFFVDEBELL 558
Db 535 PEGRGLAGPAE--FELEEELE-----ADHTPHYEQETBPPL 569
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Search completed: September 21, 2004, 22:41:15
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:38:22 ; Search time 33 Seconds
(without alignments)
1024.697 Million cell updates/sec

Title: US-10-663-157-2

Perfect score: 3456

Sequence: 1 MGTSPSSSTALASCSRIARR.....SOEASQTLLDSVYSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3456	100.0	655	US-09-527-236A-2	Sequence 2, Appli
2	3456	100.0	655	US-09-314-844F-2	Sequence 2, Appli
3	3456	100.0	655	US-09-756-854-2	Sequence 2, Appli
4	3450	99.8	655	US-08-959-382-2	Sequence 2, Appli
5	2892	83.7	605	US-09-042-785A-23	Sequence 23, Appli
6	2723	78.8	573	US-09-042-785A-2	Sequence 2, Appli
7	1359	39.3	253	US-09-042-785A-4	Sequence 4, Appli
8	841	24.3	147	US-09-527-236A-19	Sequence 19, Appli
9	841	24.3	147	US-09-756-854-19	Sequence 19, Appli
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13	431	12.5	84	US-09-042-785A-30	Sequence 30, Appli
14	431	12.5	84	US-09-042-785A-31	Sequence 31, Appli
15	352	10.2	67	US-09-527-236A-21	Sequence 21, Appli
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17	343.5	9.9	461	US-08-385-229-2	Sequence 2, Appli
18	343.5	9.9	461	US-08-650-000-2	Sequence 2, Appli
19	343.5	9.9	461	US-09-042-785A-7	Sequence 7, Appli
20	343.5	9.9	461	US-08-477-347-3	Sequence 3, Appli
21	343.5	9.9	461	US-09-006-353A-4	Sequence 4, Appli
22	343.5	9.9	461	US-08-476-862-2	Sequence 2, Appli
23	343.5	9.9	461	US-09-573-986-4	Sequence 4, Appli
24	343.5	9.9	461	US-08-406-824A-2	Sequence 2, Appli
25	343.5	9.9	461	US-09-800-909-2	Sequence 2, Appli
26	343.5	9.9	461	US-09-758-124-2	Sequence 2, Appli
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30 312.5 9.0 518 4 US-09-579-845-1 Sequence 1, Appli
31 312.5 9.0 518 4 US-09-579-845-3 Sequence 3, Appli
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41 305.5 8.8 235 4 US-09-580-235-6 Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-527-236A-2
; Sequence 2, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-2

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Best Local Similarity 100.0%; Pred. No. 2.6e-299;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTSPSSSTALASCSRIARRATATMTAGSLLLGFLSTTTAQPEQKASNLIGYRHVDRA 60
Db 1 MGTSPSSSTALASCSRIARRATATMTAGSLLLGFLSTTTAQPEQKASNLIGYRHVDRA 60

Qy 61 TQGVLTCDKCPAGTYVSEHCTNTSLRVCSCPVGVTFRHENGIEKCHDCSQPCPWPMEK 120
Db 61 TQGVLTCDKCPAGTYVSEHCTNTSLRVCSCPVGVTFRHENGIEKCHDCSQPCPWPMEK 120

Qy 121 LPCAALTDRECTPPGMFQSNATCAPHTVCPVGWGRKKGTTEDYRCKOCASGTSDVP 180
Db 121 LPCAALTDRECTPPGMFQSNATCAPHTVCPVGWGRKKGTTEDYRCKOCASGTSDVP 180

Qy 181 SSVMKCXYTDCLSQLNVLWKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPREHEMETH 240
Db 181 SSVMKCXYTDCLSQLNVLWKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPREHEMETH 240

Qy 241 VPSSTYVPKGMNSTEENSASVRPKVLSSIQEGTVFDNTSSARKCKEDVNTKLTNQLQVNH 300


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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-756-854-2

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DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGYRHHVDRA 60

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DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120

QY 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTEDVRCQKARGTFSDVP 180
DB 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTEDVRCQKARGTFSDVP 180

QY 181 SSMVKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
DB 181 SSMVKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240

QY 241 VPSSTVVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYNKLPNLQVYNH 300
DB 241 VPSSTVVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYNKLPNLQVYNH 300

QY 301 QQGPHERHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
DB 301 QQGPHERHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYCNGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYCNGHGIDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGYTADHERAYAAHQHTIRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGYTADHERAYAAHQHTIRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNAKLENSALLTVEP 540

QY 541 SPQDNKNGFFVDESEPLRCDSSTSSGSSALSNGSGFTKEKKTIVLRQVRLDPCDLQPIF 600
DB 541 SPQDNKNGFFVDESEPLRCDSSTSSGSSALSNGSGFTKEKKTIVLRQVRLDPCDLQPIF 600

QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
```

RESULT 4

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US-08-959-382-2
; Sequence 2, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR7
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAINER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

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/
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-959-382-2
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Query Match          99.8%; Score 3450; DB 3; Length 655;
Best Local Similarity 99.8%; Pred. No. 8e-299;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGYRHHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGYRHHVDRA 60

QY 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120
DB 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSGCPVGTFRHENGIEKCHDCSQPCPWPMEIK 120

QY 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTEDVRCQKARGTFSDVP 180
DB 121 LPCAALTDRCTCPGPFQSNATCAPHTVCPVGWGVKKGTTEDVRCQKARGTFSDVP 180

QY 181 SSMVKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240
DB 181 SSMVKCKAYTDCLSQNLVVIKGTETDNVCGTLPSFSSSTSPSGTAFPRPEHMETHE 240

QY 241 VPSSTVVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYNKLPNLQVYNH 300
DB 241 VPSSTVVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDYNKLPNLQVYNH 300

QY 301 QQGPHERHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360
DB 301 QQGPHERHILKLLPSMEATGGEKSTPIKGPKRGHPRQNLHKHFDINEHLPWMLVFLLL 360

QY 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYCNGHGIDILK 420
DB 361 VLWVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWTYYCNGHGIDILK 420

QY 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGYTADHERAYAAHQHTIRGPEASLAQLIS 480
DB 421 LVAAQVGSQWKDIYQFLCNASREVAAFNSGYTADHERAYAAHQHTIRGPEASLAQLIS 480

QY 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNAKLENSALLTVEP 540
DB 481 ALRQHRNDVVEKIRGLMEDTTQLETDKLALPMSPLSPSPISPNAKLENSALLTVEP 540

QY 541 SPQDNKNGFFVDESEPLRCDSSTSSGSSALSNGSGFTKEKKTIVLRQVRLDPCDLQPIF 600
DB 541 SPQDNKNGFFVDESEPLRCDSSTSSGSSALSNGSGFTKEKKTIVLRQVRLDPCDLQPIF 600

QY 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
DB 601 DMLHFLNPEELRVIEEIPQAEKDLRLFEIIGVKSQEASQTLSDSVYSHLPDLL 655
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Db 122 TKETDNCVGMELFFSSTNPPSSGTVTFSPHEMESHPVDSSTYEPQGMNSTDNSASTASVR 181
Qy 264 PKVLSSIOEGTVPDNTSSARGKEDVNTKLPNLQVNVHCQGGHHRHILKLLP-SNEATGGE 322
Db 182 TKVPEGIEEGTVPDNTSSARGKEDVNTKLPNLQVNVHCQGGHHRHILKLLPSSMEAT-GE 240
Qy 323 KSSTPIKPKRGHPRQNLKHFIDINEHLPMMIVFLLLVLVIVVCSIRKSSRTLKKGPR 382
Db 241 KSSTAIAKPKRGHPRQNLKHFIDINEHLPMMIVFLLLVLVIVVCSIRKSSRTLKKGPR 300
Qy 393 QDPSAIVKAGIKKSMSTQNRKWIYYCNGHGDILKLVAAQVGSQWKDIYQFLCNASE 442
Db 301 QDPSAIVKAGIKKSLTPTQNRKWIYYRNGHGDILKLVAAQVGSQWKDIYQFLCNASE 360
Qy 443 REVAAFSGNYTADHERAVALQHWITIRGPESLAQLISALRQHRNDVVEKIRGLMEDTT 502
Db 361 REVAAFSGNYTADHERAVALQHWITIRGPESLAQLISALRQHRNDVVEKIRGLMEDTT 420
Qy 503 QLETDKALPMSPLSPSPSPNAKLENSALLTVPEPSQDKNKGFFVDESEPLLRCD 562
Db 421 QLETDKALPMSPLSPSPSPNVKLENSALLTVPEPSQDKNKGFFVDESEPLLRCD 480
Qy 563 TSSGSSALSRGSPFTTKKKDTVLROVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAE 622
Db 481 TSSGSSALSRGSPFTTKKKDTVLROVRLDPCDLOPIFDDMLHFLNPEELRVIEEIPQAE 540
Qy 623 DKLDLRFIIIGVKSQEAQTLLDSVYSHLPDLL 655
Db 541 DKLDLRFIIIGVKSQEAQTLLDSVYSHLPDLL 573

RESULT 7
US-09-042-785A-4
; Sequence 4, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-042-785A-4

Query Match 39.3%; Score 1359; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.9e-113;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGTSPSSSTALASCSPRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
Db 1 MGTSPSSSTALASCSPRIARRATATMIAGSLLLGLFLSTTTAQPEQKASNLIGTYRHVDRA 60
Qy 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSQCPVGTFTFRHENGIEKCHDCSQPCPWPMEIK 120
Db 61 TGOVLTCDCPCAGTYVSEHCTNTSLRVCSQCPVGTFTFRHENGIEKCHDCSQPCPWPMEIK 120
Qy 121 LPCAALTDRECTCPPGMFQSNATCAPHTVCPVGMGVRKKGTTEDVRCQCARGTSDVP 180
Db 121 LPCAALTDRECTCPPGMFQSNATCAPHTVCPVGMGVRKKGTTEDVRCQCARGTSDVP 180
Qy 181 SSVMKCKATDCLSONLVVKPQTKETDNCVGTLSFSSSTSPSPCTAIFRPRPEHMETHE 240
Db 181 SSVMKCKATDCLSONLVVKPQTKETDNCVGTLSFSSSTSPSPCTAIFRPRPEHMETHE 240
Qy 241 VPSSTYVVK 249
Db 241 VPSSTYVVK 249

RESULT 8
US-09-527-236A-19
; Sequence 19, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; PRIOR APPLICATION NUMBER: 2000-03-16
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-19

Query Match 24.3%; Score 841; DB 4; Length 147;
Best Local Similarity 99.3%; Pred. No. 3.9e-67;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 66 TCDKCPAGTYVSEHCTNTSLRVCSQCPVGTFTFRHENGIEKCHDCSQPCPWPMEIKLPCAA 125
Db 1 TCDKCPAGTYVSEHCTNTSLRVCSQCPVGTFTFRHENGIEKCHDCSQPCPWPMEIKLPCAA 60
Qy 126 LTDRECTCPPGMFQSNATCAPHTVCPVGMGVRKKGTTEDVRCQCARGTSDVPSSVMK 185
Db 61 LTDRECTCPPGMFQSNATCAPHTVCPVGMGVRKKGTTEDVRCQCARGTSDVPSSVMK 120
Qy 186 CKAYTDCLSQNLVVKPQTKETDNCVCG 212
Db 121 CKAYTDCLSQNLVVKPQTKETDNCVCG 147

RESULT 9
US-09-756-854-19

```

; Sequence 19, Application US/09756954
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Yu, Guo-Liang
; Fan, Ping
; Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-756-854-19

Query Match 24.3%; Score 841; DB 4; Length 147;
Best Local Similarity 99.3%; Pred. No. 3.9e-67;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 TCCKCPAGTYVSEHCNTSLRVCSSCPVGTTRHENGIEKCHDCSQCPWPMIEKLPCAA 125
DB 1 TCCKCPAGTYVSEHCNTSLRVCSSCPVGTTRHENGIEKCHDCSQCPWPMIEKLPCAA 60

QY 126 LTDRCTCPGFMFQSNATCAHTVCPVGWYRKGTETEDVRCKOCARGTFSDDVPSSVMK 185
DB 61 LTDRCTCPGFMFQSNATCAHTVCPVGWYRKGTETEDVRCKOCARGTFSDDVPSSVMK 120

QY 186 CKAYTDCLSQNLWIKPTGKTDNVCV 212
DB 121 CKAYTDCLSQNLWIKPTGKTDNVCV 147

RESULT 10
US-08-959-382-4
; Sequence 4, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR7

```

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MOLECULE TYPE: protein
US-08-959-382-4

Query Match 19.5%; Score 673; DB 3; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.9e-52;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCRIARRATATWAGSLLLGLFLSTTTAQPEOKASNLGTYRHVDRA 60
DB 1 MGTSPSSSTALASCRIARRATATWAGSLLLGLFLSTTTAQPEOKASNLGTYRHVDRA 60

QY 61 TQVLTCDKCPAGTYVSEHCNTSLRVCSSCPVGTTRHENGIEKCHDCSQCPWPMIEK 120
DB 61 TQVLTCDKCPAGTYVSEHCNTSLRVCSSCPVGTTRHENGIEKCHDCSQCPWPMIEK 120

QY 121 LFCAA 125
DB 121 LFCAA 125

RESULT 11
US-09-314-844F-4
; Sequence 4, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; TITLE OF INVENTION: RECEPTOR TR7
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 125
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-314-844F-4

Query Match
Best Local Similarity 19.5%; Score 673; DB 4; Length 125;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLGTYRHVDRA 60
DB 1 MGTSPSSSTALASCSRIARRATATMIAGSLLLGLFLSTTTAQPEKASNLGTYRHVDRA 60

QY 61 TQVLTCDKCPAGTVVSEHCINTSLRVCSGPCVGTFTTRHENGIEKCHDCSQCPWPMIEK 120
DB 61 TQVLTCDKCPAGTVVSEHCINTSLRVCSGPCVGTFTTRHENGIEKCHDCSQCPWPMIEK 120

QY 121 LPCAA 125
DB 121 LPCAA 125

RESULT 12
US-09-314-844F-6
; Sequence 6, Application US/09314844F
; Patent No. 6860839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: RECEPTOR TRY
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-314-844F-6

Query Match
Best Local Similarity 15.9%; Score 548; DB 4; Length 102;
Matches 98; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 25 MIAGSLLLGLFLSTTTAQPEKASNLGTYRHVDRA TQVLTCDKCPAGTVVSEHCINTS 84
DB 1 MIAGSLLLGLFLSTTTAQPEKASNLGTYRHVDRA TQVLTCDKCPAGTVVSEHCINTS 60

QY 85 LRVCSGPCVGTFTTRHENGIEKCHDCSQCPWPMIEKLPCAA 125
DB 61 LRVCSGPCVGTFTTRHENGIEKCHDCSQCPWPMIEKLPCAS 101

RESULT 13
US-09-042-785A-30
; Sequence 30, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 125
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-042-785A-30

Query Match
Best Local Similarity 12.5%; Score 431; DB 3; Length 84;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTWTIRGPEAS 474
DB 1 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTWTIRGPEAS 60

QY 475 LAQLISALRQHRNDVVEKIRGLM 498
DB 61 LAQLISALRQHRNDVVEKIRGLM 84

RESULT 14
US-09-042-785A-31
; Sequence 31, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; APPLICANT: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION NUMBER: US 08/938,896
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
```

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; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION NUMBER: US 08/938,896
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-30

Query Match
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTWTIRGPEAS 474
DB 1 GIDILKLVAAQVGSQWKDIYQFLCNASEREVAAFNSGYTADHERAYAAALQHTWTIRGPEAS 60

QY 475 LAQLISALRQHRNDVVEKIRGLM 498
DB 61 LAQLISALRQHRNDVVEKIRGLM 84

RESULT 14
US-09-042-785A-31
; Sequence 31, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; APPLICANT: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION NUMBER: US 08/938,896
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-042-785A-31

Query Match 12.5%; Score 431; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GIDILKLVAAQVGSQWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEAS 474
Db 1 GIDILKLVAAQVGSQWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEAS 60

QY 475 LAQLISALRQHRNDVVEKIRGLM 498
Db 61 LAQLISALRQHRNDVVEKIRGLM 84

RESULT 15
US-09-527-236A-21
; Sequence 21, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375Pl
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-527-236A-21

Query Match 10.2%; Score 352; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 QWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEASLAQLISALRQHRN 488
Db 1 QWKDIYQFLCNASREVAAFSNGYTADHERAYAAALQHWTTIRGPEASLAQLISALRQHRN 60

QY 489 DVVEKIR 495
Db 61 DVVEKIR 67

Search completed: September 21, 2004, 22:44:42
Job time : 35 secs
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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:34:42 ; Search time 25 seconds
(without alignments)
1364.238 Million cell updates/sec

Title: US-10-663-157-2
Perfect score: 3456
Sequence: 1 MGTSPSSSTALASCRIARR.....SQEASQTLDSVYSHLPDLL 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

/ Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3456	100.0	655	1 TR21_HUMAN	Q9509 homo sapien
2	3059	88.5	655	1 TR21_MOUSE	Q9509 mus musculu
3	343.5	9.9	461	1 TR1B_HUMAN	P20333 homo sapien
4	304.5	8.8	401	1 TR1B_RAT	O08727 rattus norv
5	301.5	8.7	401	1 TR1B_HUMAN	O00300 homo sapien
6	301.5	8.7	401	1 TR1B_MOUSE	O08712 mus musculu
7	287	8.3	300	1 TR6B_HUMAN	O95407 homo sapien
8	273.5	7.9	474	1 TR1B_MOUSE	P25119 mus musculu
9	238	6.9	415	1 TRN3_MOUSE	P50284 mus musculu
10	236.5	6.8	416	1 TR16_CHICK	P18519 gallus gall
11	235.5	6.8	255	1 TRN9_HUMAN	Q07011 homo sapien
12	233	6.7	289	1 TRN5_MOUSE	P27512 mus musculu
13	228.5	6.6	435	1 TRN3_HUMAN	P36941 homo sapien
14	227	6.6	269	1 TRN5_BOVIN	Q28203 bos taurus
15	218.5	6.3	326	1 V12_MXVL	P29825 myxoma viru
16	215.5	6.2	351	1 CRMB_COWPX	P29559 cowpox viru
17	211.5	6.1	325	1 V12_SFVKA	P25943 Shope fibro
18	211.5	6.1	425	1 TR16_RAT	P07174 rattus norv
19	210.5	6.1	427	1 TR16_HUMAN	P08138 homo sapien
20	208.5	6.0	349	1 CRMB_CAMPS	Q8uy47 camelipox vi
21	206.5	6.0	349	1 CRMB_VARV	P34015 variola vir
22	206	6.0	625	1 TR11_MOUSE	Q35305 mus musculu
23	205.5	5.9	616	1 TR11_HUMAN	Q9y6g6 homo sapien
24	205	5.9	283	1 TR14_HUMAN	Q22956 homo sapien
25	205	5.9	595	1 TRN8_HUMAN	P28908 homo sapien
26	200	5.8	277	1 TRN5_HUMAN	P25942 homo sapien
27	199.5	5.8	417	1 TR16_MOUSE	Q20w1 mus musculu
28	195	5.6	471	1 TR1A_BOVIN	O19131 bos taurus
29	193	5.6	461	1 TR1A_PIG	P50555 sus scrofa
30	187.5	5.4	493	1 TRN8_RAT	P97525 rattus norv
31	186.5	5.4	461	1 TR1A_RAT	P22934 rattus norv
32	180.5	5.2	256	1 TRN9_MOUSE	P20334 mus musculu
33	176	5.1	498	1 TRN8_MOUSE	Q50846 mus musculu

34	175	5.1	176	1	TR23_MOUSE	Q9er63 mus musculu
35	170	4.9	454	1	TR1A_MOUSE	P25118 mus musculu
36	162	4.7	259	1	TR10C_HUMAN	O14798 h tumor nec
37	154	4.5	277	1	TRN4_HUMAN	P43489 homo sapien
38	149.5	4.3	1193	1	TRN2_HUMAN	Q13753 homo sapien
39	148	4.3	271	1	TRN4_RAT	P15725 rattus norv
40	146	4.2	198	1	TR22_MOUSE	Q9er62 mus musculu
41	145.5	4.2	455	1	TR1A_HUMAN	P19438 homo sapien
42	143	4.1	204	1	TR26_MOUSE	P83626 mus musculu
43	142	4.1	417	1	TR25_HUMAN	Q93038 h tumor nec
44	136	3.9	272	1	TRN4_MOUSE	P47741 mus musculu
45	135.5	3.9	5376	1	ZAN_MOUSE	O88799 mus musculu

ALIGNMENTS

RESULT 1
TR21_HUMAN
ID TR21_HUMAN STANDARD; PRT; 655 AA.
AC Q75509; Q96D86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE tumor necrosis factor receptor superfamily member 21 precursor (TNFR- related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98378343; PubMed=9714541;
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C., Aggarwal B.B., Ni J., Dixit V.M.;
RT "Identification and functional characterization of DR6, a novel death domain-containing TNF receptor."
RT FEBS Lett. 431:351-356(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
RC TISSUE=Brain, and Colon;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC -!- SUBUNIT: Associates with TRADD.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p75) (TNFR-2) (ETAR) (CD120b) (ETAR)
DE [Contains: Tumor necrosis factor binding protein 2 (TNFR2)]
GN TNFRSF1B OR TNFR2 OR TNFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90260639; PubMed=2160731;
RX Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RN SEQUENCE FROM N.A., AND VARIANT ARG-196.
RP MEDLINE=91045991; PubMed=2172983;
RX Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=96299745; PubMed=8661109;
RX Belinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RN SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
RP ARG-301.
RX Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP TISSUEPNS;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Perge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnold J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1366549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
RN [7]
RN SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [8]
RN SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=1117692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
RN [9]
RN SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [10]
RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91056048; PubMed=2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [11]
RN CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [12]
RN INTERACTION WITH TRAF2.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
RN [14]
RN VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21633988; PubMed=11762942;
RA Morita C., Horiuchi T., Tsukamoto H., Hata N., Kikuchi Y.,
RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;
RT "Association of tumor necrosis factor receptor type II polymorphism
RT 196R with systemic lupus erythematosus in the Japanese: molecular and
RT functional analysis.";
RL Arthritis Rheum. 44:2819-2827(2001).
RN [15]
RN VARIANT ARG-196.
RX MEDLINE=22151311; PubMed=12161545;
RA Peral B., San Millan J.L., Castello R., Moghetti P.,
RA Escobar-Morreale H.F.;
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic
RT ovary syndrome and hyperandrogenism.";
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).
RN [16]
RN FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and

approximately 5-fold lower affinity for homotrimeric TNF α /lymphotoxin- α . The TRAF1/IRAP2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF receptor 2 mediates most of the metabolic effects of TNF- α .

!- SUBUNIT: Binds to TRAF2.

!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.

!- PTM: Phosphorylated; mainly on serine residues and with a very low level on threonine residues.

!- PTM: A soluble form (tumor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing.

!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to TNF- α and blocks its interactions with receptors.

!- SIMILARITY: Contains 4 TNFR-Cys repeats.

!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".

!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrel.com/".

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DR EMBL; M32315; AAA59929.1; -.

DR EMBL; U52165; AAC50622.1; -.

DR EMBL; U52156; AAC50622.1; JOINED.

DR EMBL; U52157; AAC50622.1; JOINED.

DR EMBL; U52158; AAC50622.1; JOINED.

DR EMBL; U52159; AAC50622.1; JOINED.

DR EMBL; U52160; AAC50622.1; JOINED.

DR EMBL; U52161; AAC50622.1; JOINED.

DR EMBL; U52162; AAC50622.1; JOINED.

DR EMBL; U52163; AAC50622.1; JOINED.

DR EMBL; U52164; AAC50622.1; JOINED.

DR EMBL; M55994; AAA36755.1; -.

DR EMBL; AY248404; AAC89076.1; -.

DR EMBL; AY342040; AAP88939.1; -.

DR EMBL; BC052977; AAH52977.1; -.

DR EMBL; M36368; AAB19824.2; -.

DR EMBL; M35857; AAA63262.1; -.

DR EMBL; AB030950; BAA89053.1; -.

DR PIR; A35356; A35356.

DR PDB; 1CA9; 12-APR-99.

Genew; HGNC:11917; TNFRSF1B.

Query Match 9.9%; Score 343.5; DB 1; Length 461;
Best Local Similarity 29.2%; Pred. No. 2.6e-15;
Matches 95; Conservative 35; Mismatches 116; Indels 79; Gaps 11;

QY 65 LTCDKCPAGTVSEHCTNTSLRVCSQPVGTFTHRENGIEKCHDCSPCPWPMTIEKLPQCA 124

DB 52 MCCSKCSFGQAKVFCFTKTSBTDSCSDSTYTQLNWPVPECLSCGRSCSDVETQACT 111

QY 125 ALTDRECCPCPGME-----QSNATCAPHTYCPVGWGVKKGTEDEVCKQCARGTFSD 178

DB 112 REQNRICIRGOWYCALSKQGRCLCAPLRCRFGFGVARGTETSDVCKPCAPGIFSN 171

QY 179 VPSSVMKCAKAYTDLSQLNVLKPTKETDNCVGTLPFSFSSSTSP-----SPGTAIFPRP- 233

DB 172 TTSSTDICRPHQIC--NWVAI-PGNASMDAVC-----TSTSPTRSMAPGAVHLQPV 220

QY 234 ----EHEMTHEVPS-----SYVPKGMNSTESNS----- 259

DB 221 STRSOHTPTPEPSTAPSTFLLPMGPSPFPAEGSTGDFALPVGLIVGTAIGLLIIGVN 280

QY 260 ----ASVRPKVLSIQETQVDP-NTSSARGKEDVKNKTLPLNQLVNVHQGGPHRHILKLP 314

Db 281 CVMVTQVKKKPLCLOREAKVPHLPADKARG-----TQGFEOCHLLITAP 324

QY 315 SMEATGGEKSSTPI--KGPGRGHP 337

DB 325 SSSSSLESSASALDRAPTRNPQ 349

RESULT 4

TI1B_RAT ID TI1B_RAT STANDARD; PRT; 401 AA.

AC 008727;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE tumor necrosis factor receptor superfamily member 11B precursor

DE (Osteoprotegerin).

DE TNFRSF11B OR OPG.

GN TNFRSF11B OR OPG.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryonic intestine;

RC MEDLINE=97262071; PubMed=9108485;

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Daroche M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;

RT "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."

RL Call 89-309-313(1997).

CC !- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis (By similarity).

CC !- SUBUNIT: Homodimer (By similarity).

CC !- SUBCELLULAR LOCATION: Secreted (By similarity).

CC !- INDUCTION: Upregulated by osteopontin.

CC !- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC !- SIMILARITY: Contains 2 death domains.

CC -----

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CC -----

DR EMBL; U94330; AAB53707.1; -.

DR HSSP; P25942; 1CDF.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR_C6.

DR Pfam; PF00020; TNFR_C6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM02008; TNFR; 4.

DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00652; TNFR_NGFR_2; 2.

DR PROSITE; PS00650; TNFR_NGFR_2; 2.

KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B.

FT REPEAT 24 62 TNFR-CYS 1.

FT REPEAT 65 105 TNFR-CYS 2.

FT REPEAT 107 142 TNFR-CYS 3.

FT REPEAT 145 185 TNFR-CYS 4.

FT DOMAIN 198 269 DEATH 1.
 FT SITE 270 365 DEATH 2.
 FT DISULFID 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 401 AA; 46192 MW; PFC6A31FID4E573A CRC64;
 Query Match 8.8%; Score 304.5; DB 1; Length 401;
 Best Local Similarity 28.6%; Pred. No. 7.8e-13;
 Matches 91; Conservative 44; Mismatches 142; Indels 41; Gaps 9;

QY 30 LLLGLFLSTTAQ--PEQKASNLIGTVRHVDRTGQVLTCDKCPAGTVVSEHCTNTSLRV 87
 DB 10 LVFLDIETWTQETPPK-----YLHYDETRGQLLCKDCAPGYLYKQHCIVRRTL 61
 QY 88 CSSCPVGTFTRHENGIEKCHDCSPQCPWPMIEKLPFCAALTDRECTCPGPMFQSNATCAPH 147
 DB 62 CVCPCDYSYDTSWHTSDCVYCSVCKELQTVQECNTRHVRCEBEGRYLEFCLKH 121
 QY 148 TVCPGVGWVRKGTETEDVRCKQARGTFSDVPSSVMKCKAYTCLSNLVVIFPGTKET 207
 DB 122 RSCPPGLVQLAGTPEFTNVCKRCDPGFSGTSSKAPCRKHTCNSSGLGLLIQGNATH 181
 QY 208 DNVCGTLPSFSSTSPSPGTAIFPPPEHMETHEVPSSVTPVKGN-----STESNSA 260
 DB 182 DNVG-----SGNREATQNGIDVTLCEEAFFFAFVPTK-IIFNLVSLVDSLPGRKVAES 236
 QY 261 SVRPKVLISIQGTVP-----DNTSSARGKEDVNTLPLNVLQVNVQOQPHHHI---- 309
 DB 237 VERIKRRHSSQETQLKLKWHQN---RDQENVKKIIDIIDLCSSVQRHGHANLTT 292
 QY 310 --LKLPSMEATGPKSS 325
 DB 293 EQRLIL--MESLPGKKIS 308

RESULT 5

T11B HUMAN STANDARD; PRT; 401 AA.
 AC O00300; O60236; Q9UHP4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPB OR OCIF.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 Luechty R., Nguyen H.O., Woodson S., Bennett L., Boone I., Shimamoto G.,
 Derese M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 Suggs S., Boyle W.J.,
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";

RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung cancer;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 Tsuda E., Morinaga T., Higashio K.;
 RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Placenta;
 RX MEDLINE=98351869; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Eve;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Ratkovich S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richardson S., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
 Raheij J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 22-36 AND 378-401.
 RX MEDLINE=98238645; PubMed=9571159;
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
 RA Morinaga T., Tsuda E., Higashio K.;
 RT "Characterization of monomeric and homodimeric forms of
 RT osteoclastogenesis inhibitory factor.";
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
 RN [6]
 RP SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 RN [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.;
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 RN [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dadds R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";

J. Biol. Chem. 273:14363-14367(1998).

[9]

RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.

RX MEDLINE=98149058; PubMed=9478964;

RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,

RT Morinaga T., Higashio K.;

RT "Characterization of structural domains of human osteoclastogenesis

RT inhibitory factor."

RL J. Biol. Chem. 273:5117-5123(1998).

RN [10]

RP REVIEW

RX MEDLINE=21395914; PubMed=11505389;

RA Hobbauer L.C., Neubauer A., Heufelder A.E.;

RT "Receptor activator of nuclear factor-kappa ligand and

RT osteoprotegerin: potential implications for the pathogenesis and

RT treatment of malignant bone diseases.";

RL Cancer 92:460-470(2001).

CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes

CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone

CC homeostasis seems to depend on the local RANKL/OPG ratio. May also

CC play a role in preventing arterial calcification. May act as decoy

CC receptor for TRAIL and protect against apoptosis. TRAIL binding

CC blocks the inhibition of osteoclastogenesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,

CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,

CC lymph node, trachea, adrenal gland, testis, and bone marrow.

CC Detected at very low levels in brain, placenta and skeletal

CC muscle. Highly expressed in fetal kidney, liver and lung.

CC -!- INDUCTION: Upregulated by increasing calcium-concentration in the

CC medium and estrogens. Downregulated by glucocorticoids.

CC -!- PTM: N-glycosylated. Contains sialic acid residues.

CC -!- PTM: The N-terminus is blocked.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 2 death domains.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U94332; AAB53709.1; -

DR EMBL; AB002146; BAA25910.1; -

DR EMBL; AB008822; BAA32076.1; -

DR EMBL; AB008821; BAA32076.1; JOINED.

DR EMBL; BC030155; AAH30155.1; -

DR EMBL; AF134187; AAF20168.1; -

DR HSSP; P25942; ICDP. -

DR Genew; HGNC:11909; TNFRSF11B.

DR MIM; 602643; -

DR GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0005125; P:cytokine activity; TAS.

DR GO; GO:0004872; P:receptor activity; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR GO; GO:0001501; P:skeletal development; TAS.

DR InterPro; IPR000488; Death.

DR Pfam; PF00020; TNFR_c6; 3.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 2.

KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

FT SIGNAL 1 21

FT CHAIN 22 401

FT TUMOR NECROSIS FACTOR RECEPTOR

FT SUPRENFAMILY MEMBER 11B

FT REPEAT 24 62

FT TNFR-CYS 1.

FT REPEAT 65 105

FT REPEAT 107 142

FT REPEAT 145 185

FT DOMAIN 198 269

FT DOMAIN 270 365

FT SITE 400 400

FT SITE 41 54

FT DISULFID 44 62

FT DISULFID 65 80

FT DISULFID 83 97

FT DISULFID 107 118

FT DISULFID 124 142

FT DISULFID 145 160

FT DISULFID 166 185

FT CARBOHYD 98 98

FT CARBOHYD 152 152

FT CARBOHYD 165 165

FT CARBOHYD 178 178

FT CARBOHYD 289 289

FT VARIANT 3 3

FT MUTAGEN 400 400

FT MUTAGEN 400 401

FT CONFLICT 263 263

FT SEQUENCE 401 AA; 48040 MW; EDF48B67D86C71E CRC64;

Query Match 8.7%; Score 301.5; DB 1; Length 401;

Best Local Similarity 24.8%; Pred. No. 1.2e-12;

Matches 102; Conservative 58; Mismatches 177; Indels 75; Gaps 13;

QY 54 YRHVDATQVLTCDKCRAGTVVSEHCTNTSLRVCSGCPVGTFRHENGIEKHCDSQPC 113

DB 28 YLHDEETSHQLLDCDKCPPTGYLKQHCCTAKWTCVACPCDPHYTDSWHTSDECLYCSPVC 87

QY 114 PFWIEKLPAAALTDRETCPPGFMQSNATCATPTVCPVGMVGRKKGTEDEVRCQCAR 173

DB 88 KELQYVQECNRTHNRVCEKSGRYLEIEFCLKHSRCPFGVQAGTPTNVTVCRCPD 147

QY 174 GTFSDVPSSVMKCAVTDCLSONLVKGTETKTDVTCGLTSPSSSTSPSGTALFPPR 233

DB 148 GFFSNSTSKAPCRKTNCSVFGLLTQGNATHDNIC-----SGNSESTKCGIDVTLC 203

QY 234 EHMETHEVPSSTVPRKGMN-----STESNSASVRPKVLSIOBGTVP-----DNT 279

DB 204 EAFPRAVTK-FTPNWLSVLVDNLPGTKVAESVERIKRQSSQEQTQLKLWKQHN- 261

QY 280 SSARGKEDVNTKLPNLQVNVNHOOGPHRH-----ILKLLPSMEATGGEKSTPIK 329

DB 262 ---KDQDIVKVIQIDILCENSQVRHIGHANLTFEQLRSLMESLPG-KKVGAEIDIEKTIK 317

QY 330 GPKRGHPRQNLKHGFDINEHLPKMWIVLFLLLVLVWVVCISIRKSSRTLKKGPRQDPSATV 389

DB 318 ACK---PSDQILKLKLLS-----WRI-----KNGQDQTLKGLM 346

QY 390 EKAGLKKS-----MTPTQNRKWIYVNCNGHGIDIL--KLVAQVGSQWKDI 433

DB 347 H--ALKHSXTYHPKTVTQSLKTIKIRFLHSFTMYKLYQKLFLEMIGNQVQSV 396

RESULT 6

T11B MOUSE

ID T11B MOUSE STANDARD; PRT; 401 AA.

AC O08712; O70202;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11B precursor

DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).

GN TNFRSF11B OR OPG OR OCIF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehly R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Davese M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RP AND ARG-296.
RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RN [3]
RP FUNCTION.
RX MEDLINE=21060987; PubMed=10952716;
RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA Simonet W.S.;
RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT osteoclasts and prevents vascular calcification by blocking a process
RT resembling osteoclastogenesis.";
RL J. Exp. Med. 192:463-473(2000).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC intestines and calvaria. Highly expressed in decidua and placenta,
CC and in embryo.
CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC whereas expression decreases at day 11 and increases from day 15
CC to 17. On day 15 found in developing bone primordia,
CC brachiocephalic artery and ductus arteriosus, left main bronchus,
CC abdominal aorta and midgut.
CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U94331; AAB53708.1; -;
CC EMBL; AB013898; BAA28269.1; -;
CC EMBL; AB013903; BAA33388.1; -;
CC EMBL; AB013899; BAA33388.1; JOINED.
CC EMBL; AB013900; BAA33388.1; JOINED.
CC EMBL; AB013901; BAA33388.1; JOINED.
CC EMBL; AB013902; BAA33388.1; JOINED.
CC HSSP; P25942; ICDF.
CC MGD; MGI:109587; Tnfrsf11b.

DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00852; TNFR_NGFR_1; 1.
DR PROSITE; PS00850; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 283 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 138 138
FT VARIANT 161 161
FT VARIANT 165 165
FT VARIANT 288 288
FT VARIANT 296 296
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
SQ
Query Match 8.7%; Score 301.5; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 1.2e-12;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;
QY 30 LLLLFLSTTTAQQKASNLIGTVRHVDRTGQVLTCDKCPAGTYVSEHCNTSLRVCS 89
Db 10 LVLLDIIEITTOE-----TLPKYLHYDPTGTHQLCDKCAPGYLKQHTVRRKTLCV 63
QY 90 SCPVGTFTRHENGIEKCHDCSQPCWPMTIEKLPAAALTDRECTCPGPFQSNATCAPHTV 149
Db 64 PCPDHSYDTSWHTSDECVYCSVKELQSVKQECNTHNRVCECEGRLBIFFCLKHRS 123
QY 150 CPVGVGVRKKGTETEDVCKQCARGTTFSDVSSVMKXAYTDCLSQNLVWIKPGTKETDN 209
Db 124 CPFGSGVQAGPPTNTVCKKCPDGFSGSETSSKAPCIKHTNCSTFGLLIQLKGNATHDN 183
QY 210 VCGTLPSPSSSTSPSPGTAIFRPPHMETHEVPSTVYVKGWN-----STENSSASV 262
Db 184 VC-----SGNREATQCGIDVTICEAFAFFAVPTK-IIPNWLVLVDSLPGLKVAESVE 238
QY 263 RPXVLSSIQEGTVP-----DNTSARGKEDVNTKLPNLQVNHQCGPHRH-----ILK 311
Db 239 RIKRHSSEQETFFQLKLWQHQN-----RDQEMVKKIIQIDLCSSVQRHGHSLNLTTEQ 294
QY 312 LLPSVEATGGEKSS 325
Db 295 LLALMESLPGKKIS 308


```

RESULT 7
TR6B HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (Dcr3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Borstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carroll P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska K., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT

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CC and TNFSF6/FasL. Protects against apoptosis.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC Detected in adult stomach, spinal cord, lymph node, trachea,
CC spleen, colon and lung. Highly expressed in several primary tumors
CC from colon, stomach, rectum, esophagus and in SW480 colon
CC carcinoma cells.
CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF104419; AAD03056.1; -
CC EMBL; AF134240; AAD29688.1; -
CC EMBL; AF217796; AAF35244.1; -
CC EMBL; AF217793; AAF33685.1; -
CC EMBL; AF217794; AAF33686.1; -
CC EMBL; AL121845; CAC03668.1; -
CC EMBL; BC017065; AAI17065.1; -
CC EMBL; BC034349; AAI34349.1; -
CC HSP; O14763; IDOG.
CC Genew; HGNC:11921; TNFRSF6B.
CC MIM; 603361; -
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:000189; F:apoptosis inhibitor activity; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PFO020; TNFR_C6; 4.
CC SMART; SMC0208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 300
FT REPEAT 31 70 TUMOR NECROSIS FACTOR RECEPTOR
FT REPEAT 72 113 SUPERFAMILY MEMBER 6B.
FT REPEAT 115 150 TNFR-CYS 1.
FT REPEAT 152 193 TNFR-CYS 2.
FT REPEAT 152 193 TNFR-CYS 3.
FT REPEAT 152 193 TNFR-CYS 4.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 52 70 BY SIMILARITY.
FT DISULFID 73 88 BY SIMILARITY.
FT DISULFID 91 105 BY SIMILARITY.
FT DISULFID 95 113 BY SIMILARITY.
FT DISULFID 115 126 BY SIMILARITY.
FT DISULFID 132 150 BY SIMILARITY.
FT DISULFID 153 168 BY SIMILARITY.
FT DISULFID 174 193 BY SIMILARITY.
FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;
Query Match 8.3%; Score 287; DB 1; Length 300;
Best Local Similarity 34.3%; Pred. No. 7.5e-12;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;
QY 53 TYRHVDRATGOVLTCDCPAGTVVSEHCTNTSLRVCSQCPVGTFTRHENGIEKCHDCSQP 112
DB 35 TYWRDAETGERLVCAQCPGTFVQPCRDPTTCGPPCPPHYTOFWNYLERCYCNVL 94
QY 113 CPNEMIEKLPFAALTDRCTCPGPMFSQSNATCAPIHTVCPVGMVRRKGTETEDVRCKQA 172
DB 95 CGREBEARACHATHNRCRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQCP 154
QY 173 RGTFSVDPVSSVMKRAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSST 221
DB 155 PGTFSSSSSSSEQCQPHRNCNTALGLALNVPGSSSHDTLCSTCTGFFLST 203

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RESULT 8
 TRIB_MOUSE STANDARD; PRT; 474 AA.
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (TNF-R2) (p/5).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor."
 RL Mol. Cell. Biol. 11:3020-3026 (1991).
 RN [3]
 RP SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN=NOD;
 RA Jacob C.O., Liu J.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=Liver;
 RA Kissinger M., Fellows R., Feldmann M., Chernajovsky Y.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
 CC approximately 5-fold lower affinity for homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The TRAF1/IRAF2 complex recruits the
 CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
 CC similarity).
 CC -!- SUBUNIT: Binds to TRAF2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 CC EMBL; M60469; AAA39752.1; -
 CC EMBL; M59378; AAA40463.1; -
 CC EMBL; U39488; AAA85021.1; -
 CC EMBL; X87128; CAA60618.1; -
 CC PIR; B38634; B38634.
 CC HSP; P19438; INCF.
 CC MGD; MGI:1314883; Tnfrsf1b.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0008220; P:necrosis; IMP.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 4-
 CC SMART; SM00208; TNFR_4
 CC PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS00650; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 1B.
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 259 288 POTENTIAL.
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 39 77 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 120 184 TNFR-CYS 3.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;
 Query Match 7.9%; Score 273.5; DB 1; Length 474;
 Best Local Similarity 25.0%; Pred. No. 1e-10;
 Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;
 QY 65 LTCDCKPCAGTYVSEHCTNTSLVSCSPGVGTFTRHENGIEKCHDCSQCPWPMIEKLPFA 124
 Db 53 MCCAKCPQGYVKEFCNKITSPTVCADCEASMYTQVWQFRTCLSCSSCTTDQVEIRACT 112
 QY 125 ALTDRECTPPGPMFQSNAT-----CAPHTVCPVGMGVKKGKTEDEVRCQKARGTF 177
 Db 113 KQNRVCAEAGRYCALKTHSSCQCVRKSKGFGVASSRAPNGNVLCACAPGTF 172
 QY 178 DVPSSVMKCKAYTDCLSQNLVVIKPTKTDNVCTLPFSFSSSTSPSGTAIFRPERHME 237
 Db 173 DTTSTTDVCRPHRIC---SILAIPGNASTDAVCA-----PESPT 208
 QY 238 THEVPSSTVY---PKGMNSTESNSSASVRPKVLSIOEGTVPDNTSSARGKEDVNTKLP 293
 Db 209 LSAIPRLVVSQPEPTRSQPLDQEPGQTSILTSL--GSTPIEQSTKG---GISLP 262
 QY 294 -----NLQVYN-----HQQGH-----HRHLK 311
 Db 263 IGLIVGVTSLGLMLGLVNCILVQKKPKSLQORDAKVPHVDPDEKSDAVGLEQOHLIT 322
 QY 312 LLPSVEATGGEKSSST--PIKGPGRGHR 337
 Db 323 TAPSSSSSSLESSASAGDRRAPPGGHQ 350
 RESULT 9
 TNFR3_MOUSE STANDARD; PRT; 415 AA.
 AC F50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072604; PubMed=7594541;

Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 Browning J.L., Ware C.F.;
 "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression.";
 J. Immunol. 155:5280-5288 (1995).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=96163885; PubMed=8586432;
 Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 Honjo T.;
 "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 sequence trap and chromosomal mapping.";
 Genomics 30:312-319 (1995).
 [3]
 INTERACTION WITH TRAF5.
 STRAIN=BALB/c;
 MEDLINE=96278943; PubMed=8663299;
 Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 Yagita H., Okumura K.;
 "TRAF5, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor";
 J. Biol. Chem. 271:14661-14664 (1996).
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs
 (By similarity).
 CC -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 CC EMBL; U29173; AAA68964.1; -.
 CC EMBL; L38423; AAB00846.1; -.
 CC EMBL; U30798; AAB81334.1; -.
 CC HSP; O14763; 1DQG.
 CC MGD; MGI:104875; ltblr.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 3.
 CC SMART; SM00208; TNFR; 3.
 CC PROSITE; PS00652; TNFR_NGFR 1; 2.
 CC PROSITE; PS00500; TNFR_NGFR 2; 3.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 CC SIGNAL 1 30
 CC CHAIN 31 415
 CC
 CC DOMAIN 31 223
 CC TRANSMEM 224 244
 CC DOMAIN 245 415
 CC REPEAT 42 81
 CC REPEAT 82 124
 CC REPEAT 125 170
 CC REPEAT 171 213
 CC REPEAT 43 58
 CC DISULFID 59 72
 CC DISULFID 62 80
 CC DISULFID 83 98
 CC DISULFID 101 116
 CC DISULFID 104 124
 CC DISULFID 126 132
 CC DISULFID 139 150
 CC DISULFID 142 169
 CC DISULFID 172 187
 CC CARBOHYD 40 40
 CC CARBOHYD 179 179
 CC SEQUENCE 415 AA; 44956 MW; 29B326A56ABEF61 CRC64;

Query Match 6.9%; Score 238; DB 1; Length 415;
 Best Local Similarity 23.5%; Pred No. 1.9e-08;
 Matches 95; Conservative 40; Mismatches 144; Indels 126; Gaps 17;
 QY 16 RIARATATMIAGSLLILGLFTTTTAQPEQKASNIIGYRHVDRA-----GV 64
 Db 2 RLPRASSPCGLAWGLLLGLSLVASQP-----LVPPYR- IENQTCWDQDKEYEYPMHD 56
 QY 65 LKCDKCPAGTYVSEHCTNTSLKVCSCPVGTTRHENGIEKCHDCSQCPWPM--IEKLP 122
 Db 57 VCSRCPPGFEFVAVCSQDVTCKTCHNSNEHNLSTCLC-RPCDIVLGEEVAP 115
 QY 123 CAALTDRECTPPGM---FQSN-----ATCAPHTVCPVGMVKKKGTTETE----- 164
 Db 116 CTSRKAECRCOPGMSCVYLDNECVHCEERLVLPQ-----GTEAEVTDEI 162
 QY 165 ---DYRCKOCARGTSDVPSSVMKCKAYTDCLSQNLVLIKPGTKTDNVCGTLPS----- 216
 Db 163 MDTVNCVPCPKGHFQNTSSPRARQCFHTRCISQGLVEAAPGTYSYDITCKNPPPGAML 222
 QY 217 -----FSS-----STSPSPGTAIFRPEHEMTHETHEVPSSTYVPRGMNS 253
 Db 223 LLAILLSLVLLFTTVLACAMWRHPSLCRKLGLTLKRHPGEESPPCPAPRADPH---- 278
 QY 254 TESNSASVRPKVLSSIQGTVP---DNTSSARGKEDVKNITLNL-QVNVHQQGP----- 304
 Db 279 -----FPDLAEPLPMSGDLSPSPAGP-----PTAPSLVEVLQQOQLVQAR 321
 QY 305 -----HHRHILKLLPSMEATGKESST-----PIKGPGRG 334
 Db 322 ELEAEPEGHQVANGANGHVTGGSVTGNIIYNGPVLGGTRG 366
 RESULT 10
 TR16 CHICK
 ID TR16 CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp90-LNGFR)
 DE (p75 ICD) (low affinity neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90166579; PubMed=2560385;
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system.";
 RL Neuron 2:1123-1134 (1989).
 RN [2]
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE=90152140; PubMed=2154393;
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.";
 RL Dev. Biol. 137:287-304 (1990).
 CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC and NT-4. Can mediate cell survival as well as cell death of
 CC neural cells (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and TRAF3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: N- and O-glycosylated.

CC -!- PTM: Phosphorylated on serine residues.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 1 death domain.
 DR PIR; JN0006; JN0006.
 DR HSP; P07174; INGR.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00652; TNFR_NGFR_2; 3.
 DR PROSITE; PS00050; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 KW Repeat; Phosphorylation; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 416
 FT
 FT DOMAIN 29 239
 FT TRANSMEM 240 261
 FT DOMAIN 262 416
 FT REPEAT 23 57
 FT REPEAT 58 99
 FT REPEAT 100 138
 FT REPEAT 140 180
 FT DOMAIN 333 410
 FT DOMAIN 188 236
 FT DISULFID 24 35
 FT DISULFID 36 49
 FT DISULFID 39 56
 FT DISULFID 59 75
 FT DISULFID 78 91
 FT DISULFID 81 99
 FT DISULFID 101 114
 FT DISULFID 117 130
 FT DISULFID 120 138
 FT DISULFID 141 156
 FT DISULFID 159 172
 FT DISULFID 162 180
 FT CARBOHYD 52 52
 FT CONFLICT 36 36
 FT CONFLICT 173 173
 FT CONFLICT 276 276
 FT CONFLICT 396 396
 SQ SEQUENCE 416 AA; 44654 MW; 6BCEAAB54F4D2D56 CRC64;

Query Match 6.8%; Score 236.5; DB 1; Length 416;
 Best Local Similarity 23.2%; Pred. No. 2.4e-08;
 Matches 105; Conservative 50; Mismatches 191; Indels 107; Gaps 15;

QY 67 CDKCPAGTYVSEHCTNTSLRVCSHC-PVGTETRHENGIEKCHDCSQPCPWFMIKLPCAA 125
 Db 36 CKACNLGGGVQPC-GVNQTVCEPCLDSVTYSATEPCPKCTQ-CVGLHSMSPACVE 93
 QY 126 LTDRCTCPGFMQS--NATCAPTVGVGVGRKGTETEDVRCKCARGTSDVPSSV 183
 Db 94 SDDAVRCAYGYFDELGSGCKECSICEVGFGLMFPQCDQSDTVCEBCEGTFDEANFV 153
 QY 184 MKCRAYTDCLSQNLVWIKPGFKETDNVCGTL-----PSFSSTSPSPGTAFIPPEH 235
 Db 154 DPCLPTIC-BENEMVKECATSDAECRDLPHTWTHPSLAGSDSPETITRDPNTEG 212
 QY 236 MTEHVPSTTVPKGMNSTENSGAS-----VRPKVLSIQEGTVPDNTSSARKEDVNKT 291
 Db 213 NATTLADIVTTVMGSSQPVWGRGTADNLIPYVCISILAAVVGVLVAYIAFKRWNSCKONKQ 272
 QY 292 LPNLQVNVHQPHRHLKLLPSMEATGGGSKSTPIKPGRGHPRGNLKHKFDINEHLP 351
 Db 273 GANRPVNTSPSPE-----GK-----LHSDSGI----- 296
 QY 352 WNVLFLLLVLIWVGVCSIRKSSRLKGPQDPSAIVEX--AGLKSMPTTQNRKWIY 409

Db 297 -----SVDSQSLHDQPPNOSTGDPAPKGDGSLYASLPSPKQEE----- 335
 QY 410 YCNGHGIDILKLVAAQGVGSQWKDIYQFLCNASEREVAAFSGY-----TADHERAYA 461
 Db 336 -----VEKLSSABETWRQL-----AGELGYKEDLLDCFTRESPARA 374
 QY 462 ALOHWITRGPBEASLAQLISALRQHRRNDVVEKI 494
 Db 375 LLADMSAK-ETATLDALLVALRKIQRGDIAESL 406

RESULT 11
 TNFR_HUMAN
 ID TNFR_HUMAN STANDARD; PRT; 255 AA.
 AC Q07011;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
 DE ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
 DE (CD137 antigen).
 GN TNFRSF9 OR ILA OR CD137.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=94374434; PubMed=8088337;
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
 Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
 RT "Molecular and biological characterization of human 4-1BB and its
 RT ligand".
 RL Eur. J. Immunol. 24:2219-2227(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=94085794; PubMed=8262389;
 RA Schwarz H., Tuckwell J., Lotz M.;
 RT "A receptor induced by lymphocyte activation (ILA): a new member of
 RT the human nerve-growth-factor/tumor-necrosis-factor receptor
 RT family".
 RL Gene 134:295-298(1993).
 RN [3]
 RP REVISION TO 107.
 RA Schwarz H.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95347766; PubMed=7622190;
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
 RA Kwon B.S.;
 RT "Characterization of human homologue of 4-1BB and its ligand".
 RL Immunol. Lett. 45:67-73(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Pearce A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussidi T.B., Teshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7].
RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.
RX MEDLINE=98078711; PubMed=9418902;
RA Arch R.H., Thompson C.B.;
RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve
RT growth factor receptor subfamily that bind TNF receptor-associated
RT factors and activate nuclear factor kappaB.";
RL Mol. Cell. Biol. 18:558-565 (1998).
RN [8].
RP INTERACTION WITH TRAF1 AND TRAF2.
RX MEDLINE=98270914; PubMed=9607925;
RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
RA Watts T.H.;
RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
RT 4-1BB ligand.";
RL J. Exp. Med. 187:1849-1862 (1998).
RN [9].
RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX MEDLINE=2162677; PubMed=11804328;
RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in
RT 4-1BB-mediated signal transduction.";
RL Mol. Cells 12:304-312 (2001).
CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC cell activation.
CC -!- SURUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with
CC LRR-repeat protein 1/LRR-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
CC -----
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CC -----
DR EMBL; U03397; AAA53133.1; -;
DR EMBL; L12964; AAA62478.2; -;
DR EMBL; AL009183; CAB57398.1; -;
DR EMBL; BC006196; AAH06196.1; -;
DR PIR; I38426; I38426
DR Genbank; HGNC:11924; TNFRSF9.
DR MIM; 602250; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; P:receptor activity; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 9.

FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT REPEAT 17 45 TNFR-CYS 1.
FT REPEAT 47 86 TNFR-CYS 2.
FT REPEAT 87 118 TNFR-CYS 3.
FT REPEAT 119 159 TNFR-CYS 4.
FT DOMAIN 214 255 INTERACTS WITH LRR-1.
FT DISULFID 28 37 BY SIMILARITY.
FT DISULFID 31 45 BY SIMILARITY.
FT DISULFID 48 62 BY SIMILARITY.
FT DISULFID 65 78 BY SIMILARITY.
FT DISULFID 68 86 BY SIMILARITY.
FT DISULFID 88 94 BY SIMILARITY.
FT DISULFID 99 106 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 121 133 BY SIMILARITY.
FT DISULFID 139 158 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;
Query Match 6.8%; Score 235.5; DB 1; Length 255;
Best Local Similarity 30.4%; Pred. No. 1.4e-08;
Matches 63; Conservative 24; Mismatches 77; Indels 43; Gaps 8;
QY 25 MIAGSLLGLGFTTAAQPEQKASNLIGTYRHVDRTGQVLTCDCPKAGTYVSEHCNTS 84
DB 8 IVATLLLVLFNFRTRSLQD-----PCSNCPAGTF-----CDNNR 41
QY 85 LRVCSGPCVGTFTRHENGIEKHCHDCSOPCPWPMEIKLPAAALTDRECTCPGWFQSNATC 144
DB 42 NQICSPCPNSFS-SAGGORTDCIQ-CGVFRTRKESSTSNAECDCITPFHCLGAGC 99
QY 145 AP-HTVCPYGVGVRKGTETEDVRCKQARGTFSDVFPSSVMKCKAYTDCLSNLVVIKPG 203
DB 100 SMCEQDCKGQELTKKG-----CKDCCFGTNDQKRGII--CRPWTNCSLDGKSVLVNG 150
QY 204 TKETDNVCGTLPS-----ESSSTSPSP 225
DB 151 TKERDVVCGFSPADLSPGASSVTPFPAP 177
RESULT 12
TNRS MOUSE
ID -TNRS_MOUSE STANDARD; PRT: 289 AA.
AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626 (1992).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/c;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=93094586; PubMed=1281194;

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaifanet M., Cassman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RL transcribed sequences derived from a somatic cell hybrid.";
RN Genomics 16:214-218(1993).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2338257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buote K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8711323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
[4]
RP CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RL death in HeLa cells.";
RN J. Biol. Chem. 274:11868-11873(1999).
[5]
RP FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RL light-mediated apoptosis of tumor cells.";
RN J. Biol. Chem. 275:14307-14315(2000).
[6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=96278943; PubMed=8663299;
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
RL the lymphotoxin-beta receptor.";
RN J. Biol. Chem. 271:14661-14664(1996).
[7]
RP INTERACTION WITH TRAF4.
RX MEDLINE=98289299; PubMed=9626059;
RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA Gascoyne R.D., Berern K., McFadden D., Shabal A., Hugh J.,
RA Reynolds A., Cleveland C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RL adult, fetal, and tumor tissues.";
RN Am. J. Pathol. 152:1549-1561(1998).
[8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA

RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RL tumor necrosis factor receptor-associated factor 5 (TRAF5).";
CC Gene 207:135-140(1998).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNF514/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC
CC EMBL; L04270; AAA36757.1; -;
CC EMBL; BC026262; AAH26262.1; -;
CC PIR; I54182; I54182.
CC HSPSP; P25942; ICDF.
CC GENE; HGNC:16718; LTR.
CC MIM; 600979; -;
CC GO; CO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR c6.
CC Pfam; PF00020; TNFR c6; 4;
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4;
CC PROSITE; PS00652; TNFR_NGFR_1; 2;
CC PROSITE; PS00505; TNFR_NGFR_2; 3;
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 30 POTENTIAL.
CC CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR
CC FT SUPERFAMILY MEMBER 3.
CC FT EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 31 227 POTENTIAL.
CC FT TRANSMEM 228 248 CYTOPLASMIC (POTENTIAL).
CC FT REPEAT 42 81 TNFR-CYS 1.
CC FT REPEAT 82 124 TNFR-CYS 2.
CC FT REPEAT 125 168 TNFR-CYS 3.
CC FT REPEAT 169 211 TNFR-CYS 4.
CC FT DISULFID 43 58 BY SIMILARITY.
CC FT DISULFID 59 72 BY SIMILARITY.
CC FT DISULFID 62 80 BY SIMILARITY.
CC FT DISULFID 83 98 BY SIMILARITY.
CC FT DISULFID 101 116 BY SIMILARITY.
CC FT DISULFID 104 124 BY SIMILARITY.
CC FT DISULFID 126 132 BY SIMILARITY.
CC FT DISULFID 139 148 BY SIMILARITY.
CC FT DISULFID 142 167 BY SIMILARITY.
CC FT DISULFID 170 185 BY SIMILARITY.
CC FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 435 AA; 624626B6022F656F CRC64;
Query Match 6.8%; Score 228.5; DB 1; Length 435;
Best Local Similarity 30.9%; Pred. No. 8.4e-08;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;
Qy 65 LTCDCPCAGTYVSEHTNTSLRYCSCPCVGTFTFRHENGIEKCHDCSQPC-PWPMEKL-P 122
Db 57 ICSCRCPGTYVSAKSRDITVCATCAENSYNEHWNLTICQLC-RPCDPVWGLEIAP 115
Qy 123 CAALTIRECTCTPCPFQMSNATCAPHTV-----CPVGVGRVKKGTETE----- 164
Db 116 CTSKRKTQCRQCPGMF-----CAWALECTHCELLSDCP-----PGTEAEELKDEVGK 163
Qy 165 DVRCQCARCTFSDVPSSVMKCKAYTDCLSQNLAVTKPGTKETDNYCGT-----LPSFSS 220

Wed Sep 22 09:32:15 2004

Receptor; Glycoprotein; Repeat; Signal.	1	16	POTENTIAL.
SIGNAL	17	326	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
CHAIN	27	62	TNFR-CYS 1.
REPEAT	63	104	TNFR-CYS 2.
REPEAT	105	147	TNFR-CYS 3.
REPEAT	148	186	TNFR-CYS 4.
REPEAT	28	39	BY SIMILARITY.
DISULFID	40	53	BY SIMILARITY.
DISULFID	43	61	BY SIMILARITY.
DISULFID	64	79	BY SIMILARITY.
DISULFID	82	96	BY SIMILARITY.
DISULFID	86	104	BY SIMILARITY.
DISULFID	106	120	BY SIMILARITY.
DISULFID	123	146	BY SIMILARITY.
DISULFID	129	149	BY SIMILARITY.
DISULFID	164	185	BY SIMILARITY.
CARBOHYD	66	66	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	181	181	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	238	238	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	326 AA;	35208 MW;	ABB027E947232FF CRC64;
Query Match	6.3%;	Score 218.5;	DB 1; Length 326;
Best Local Similarity	36.8%;	Pred. No. 2.6e-07;	
Matches	50;	Conservative 10;	Mismatches 69; Indels 7; Gaps 2;
Qy	65	LTCDKCPAGYVSEHCTNLSLRVCSCCPVGTTRHENGIEKCHDCSPCPMPMEIKLP	CA 124
Qy	38	LCCTSCPGYASRLCPGSDTVCSCKNETTASTNHAPACVSCRGCTGHLSSES	CD 97
Qy	125	ALTDRECTCPFGNF-----QSNATCAPHTVCPVGWGRKKGTTEDVRCKQCARGH	FD 178
Qy	98	KTRDRVDCGAGNYCLLKGGEGRCICAPKTKCPAGYGV-SGHTRTGDLCTKCPRTYSD	156
Qy	179	VPSSVMKCKAYTDCLS	194
Qy	157	AVSSTETCTSSFNYS	172

Search completed: September 21, 2004, 22:41:46
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 22:35:52 ; Search time 130 Seconds
(without alignments)
1589.726 Million cell updates/sec

Title: US-10-663-157-2
Perfect score: 3456
Sequence: 1 MGTPSSSTALASCRIARR.....SQBASQTLLDSVSHLPDLL 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_undefined.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2715	78.6	573	11 Q8BZU6	Q8BZU6 mus musculus
2	2356	68.2	651	13 Q98SM6	Q98SM6 gallus gall
3	453	13.1	132	13 Q90Y18	Q90Y18 salvelinus
4	354	10.2	83	13 Q8UWJ0	Q8UWJ0 gallus gall
5	326.5	9.4	457	4 Q8IVS6	Q8IVS6 homo sapien
6	308	8.9	285	13 Q90W71	Q90W71 oncorhynch
7	307	8.9	285	13 Q90V56	Q90V56 oncorhynch
8	281.5	8.1	474	11 Q80WY6	Q80WY6 rattus norv
9	278	8.0	186	13 Q7ZZY5	Q7ZZY5 gallus gall
10	277	8.0	483	13 Q800K7	Q800K7 paralicthy
11	275.5	8.0	433	11 Q91ZM6	Q91ZM6 rattus norv
12	275.5	8.0	459	11 Q623Z7	Q623Z7 mus musculus
13	268.5	7.8	302	13 Q9PU50	Q9PU50 salvelinus
14	262.5	7.6	482	11 Q88734	Q88734 mus musculus
15	262	7.6	467	13 Q800I0	Q800I0 gallus gall
16	259.5	7.5	275	11 Q80WM9	Q80WM9 mus musculus

17	257	7.4	462	13 Q805B0	Q805B0 gallus gall
18	250	7.2	274	6 Q7YRL5	Q7YRL5 canis fami
19	248.5	7.2	167	12 Q8UYL3	Q8UYL3 vaccinia vi
20	248.5	7.2	167	12 Q72762	Q72762 cowpox viru
21	240.5	7.0	167	12 Q9DJU2	Q9DJU2 cowpox viru
22	240.5	7.0	318	13 Q7T2H3	Q7T2H3 encornynch
23	238	6.9	351	12 Q57117	Q57117 cowpox viru
24	237.5	6.9	360	12 Q57118	Q57118 cowpox viru
25	233	6.7	351	12 Q57121	Q57121 cowpox viru
26	232.5	6.7	347	12 Q57119	Q57119 cowpox viru
27	231	6.7	146	13 Q7ZZY4	Q7ZZY4 gallus gall
28	231	6.7	277	6 Q8WMQ2	Q8WMQ2 ovis aries
29	231	6.7	289	11 Q8K2X6	Q8K2X6 mus musculu
30	230.5	6.7	349	12 Q57100	Q57100 monkeypox v
31	230	6.7	348	12 Q57108	Q57108 monkeypox v
32	230	6.7	348	12 Q57277	Q57277 monkeypox v
33	230	6.7	348	12 Q57103	Q57103 monkeypox v
34	228.5	6.6	349	12 Q57102	Q57102 monkeypox v
35	228	6.6	347	12 Q57115	Q57115 cowpox viru
36	227.5	6.6	349	12 Q57101	Q57101 monkeypox v
37	227.5	6.6	349	12 Q57291	Q57291 monkeypox v
38	227	6.6	278	6 Q8SQ34	Q8SQ34 sus scrofa
39	226	6.5	317	13 Q8JFV6	Q8JFV6 brachydanio
40	225.5	6.5	349	12 Q57099	Q57099 monkeypox v
41	225	6.5	355	12 Q85308	Q85308 cowpox viru
42	223.5	6.5	350	12 Q57116	Q57116 cowpox viru
43	221.5	6.4	349	12 Q57305	Q57305 cowpox viru
44	216.5	6.3	326	12 Q57120	Q57120 cowpox viru
45	214.5	6.2	326	12 Q57122	Q57122 cowpox viru

ALIGNMENTS

RESULT 1

Q8BZU6 PRELIMINARY; PRT; 573 AA.
AC Q8BZU6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Death receptor 6.
GN TNFRSF21 OR AA959878.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK033529; BAC28342.1; -.
DR MGD; MGI:2151075; Tnfrsf21.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SMC0005; DEATH; 1.
DR SMART; SMC0208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 573 AA; 63506 MW; BC883B4EC8F2FE94 CRC64;

Query Match 78.6%; Score 2715; DB 11; Length 573;
Best Local Similarity 89.9%; Pred. No. 1.4e-218;

Matches 515; Conservative 16; Mismatches 40; Indels 2; Gaps 2;

QY 84 SLRVSSCPVGTFTRENGIERKCHDCSQCPWPMIEKLPALATDRECTCPGFMFSNAT 143
 DB 2 SLRVSSCPAGTFTRENGIERKCHDCSQCPWPMIERLPALATDRECTCPGMYQNGT 61

QY 144 CAPHTVCPVGVGRKKGTTEDVRCKQACARTFSDVSSVMKCKAYTDCLSQNLVILKPG 203
 DB 62 CAPHTVCPVGVGRKKGTTEDVRCKQACARTFSDVSSVMKCKAHTDCLGQNLVILKPG 121

QY 204 TKETDNVCGTLPFSFSSSTSPSPGTAIFPRPEHMETHEVPSYVYVPGKMNSTESNSSASVR 263
 DB 122 TKETDNVCGMLFFSSTNPPSSGTVTFSHPEHMDVPSYVYVPGKMNSTDSNSTASVR 181

QY 264 PKVLSIOEGVDPNTSSARGKEDVNTLPLNLOVNHQGGPHRHILKLP-SWEATGGE 322
 DB 182 TKVPSGIEEGVDPNTSSGKEGNTLPLNPPQVTHQAPPHRHILKLPSSMEAT-GE 240

QY 323 KSSTPIKGPGRGHPRQNLKHFDINEHLPWMIVLFLLLVLIIVVCSIRKSSRTLKKGPR 382
 DB 241 KSSTAIPKGPGRGHPRQNAKHFDINEHLPWMIVLFLLLVLIIVVCSIRKSSRTLKKGPR 300

QY 383 QDPSAIVKAGLKKMTQNTONREKWIYCNCGHGDILKLVAAQVGSQWKDIYQFLCNASE 442
 DB 301 QDPSAIVKAGLKKSLTQNTONREKWIYCNCGHGDILKLVAAQVGSQWKDIYQFLCNASE 360

QY 443 REVAFAFNGYTADHERAYAAHQHTIRGPEASLAQLISALQHRNDVVEKIRGLMEDTT 502
 DB 361 REVAFAFNGYTADHERAYAAHQHTIRGPEASLAQLISALQHRNDVVEKIRGLMEDTT 420

QY 503 QLETDKALPMSPLSPSPSPNAKLENSALLTVEPSPQDKNGKGFVDESEPLLRCD 562
 DB 421 QLETDKALPMSPLSPSPSPNVKLENSTLLTVEPSPDLKNGKCFVDESEPLLRCD 480

QY 563 TSSGSSALSRNGSFITKEKKDTVLROVELDPCDLOPIFDDMLHLPNPEELRVIEEIPQAE 622
 DB 481 TSSGSSALSRNGSFITKEKKDTVLROVELDPCDLOPIFDDMLHLPNPEELRVIEEIPQAE 540

QY 623 DKDLRFLFIIGVKSQEASQTLSDSVYSHLPDLL 655
 DB 541 DKDLRFLFIIGVKSQEASQTLSDSVYSHLPDLL 573

RESULT 2
 Q98SM6
 ID Q98SM6 PRELIMINARY; PRT; 651 AA.
 AC Q98SM6;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Death receptor 6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "Expression of DR6 in the ovary."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349908; AAK29666.2; --
 DR PIR; JC7705; JC7705.
 DR HSP; P19438; INCF.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00500; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 68.2%; Score 2356; DB 13; Length 651;
 Best Local Similarity 70.8%; Pred. No. 2.1e-188; Indels 46; Gaps 10;
 Matches 470; Conservative 47; Mismatches 101;

QY 23 ATMIAGSLLLGLSTTTTAQP----EQKASNL-ICTYRHVDRATQVLTCDCPKAGTYS 77
 DB 3 AAVLAALVLLVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATQELICDKCPAGTYS 62

QY 78 EHCWTSLRVCSGCPVGTFTRENGIERKCHDCSQCPWPMIEKLPALATDRECTCPGM 137
 DB 63 KHCSTSLRECPGCPDGTFTRENGIERCHPCKPELFMIKHTCTALTIRECTCLSGT 122

QY 138 FGSNATCAPHTVCPVGVGRKKGTTEDVRCKQACARTFSDVSSVMKCKAYTDCLSQNL 197
 DB 123 FQINTCVPYTVCPVGVGRKKGTTEDVRCKPCLRGTFSDVSSVMKCKYTDGFGNM 182

QY 198 VIKSGTETDNVCG---TLP--SFSSSTSPSPGTAIFPRPEHMETHEVPSYVYVPGKMN 252
 DB 183 VVVKPGTKESDNVCGSPASLNTSLTSSDAQDG-----ETYEAPPTAYLPKGLN 232

QY 253 STESNSSASVRPKVLSIOEGVDPNTSSARGKEDVNTLPLNLOVNHQGGPHRHILKL 312
 DB 233 SVFLDSSSPAPRVNNGTAETVDTNDTSANGTVGAPGSLSSAGTAGAQAQSYRKHSTQA 292

QY 313 L---PSMEATGGEKSTPIKGPGRGHPRQNLKHFDINEHLPWMIVLFLLLVLIIVVCS 369
 DB 293 MGKQPAQEMAGGEKSSIPYRPPRGPP--NVHQHFDINEHLPWMIVLFLLLVLIIVVCS 350

QY 370 IFKSRTLLKGPQDPSAIVKAGLKKMTQNTONREKWIYCNCGHGDILKLVAAQVGSQ 429
 DB 351 VKKSRTLLKGPQDPSAIVKALNKKSTTTQNTONREKWIYCNCGHGDILKLVAAQVGSQ 410

QY 430 WKDIYQFLCNASEREVAAFNSGYTADHERAYAAHQHTIRGPEASLAQLISALQHRND 489
 DB 411 WKDIYQFLCNASEREVAAFNSGYAADHERAYAAHQHTIRGPEASLAQLISALQHRND 470

QY 490 VVEKIRGLMEDTT-----QLETDKALPMSPLSPSPSPIPSPNAKLE 531
 DB 471 VVEKIRGLMEDTTPVQMQPQWQDCSNDGDKLALFVSPSPSPVPTSP--KPP 528

QY 532 NSALLTVEPSPQDKNGKGFVDESEPLLRCDSTSSGSSALSNGSFITKEKKDTVLROVRL 591
 DB 529 DAANLTVEPSPSEK-KCFVDESEPLLRCDSTSSGSSALSRTSGFITKEKKDTVLROVRL 587

QY 592 DPCDLOPIFDDMLHLPNPEELRVIEEIPQAEKDLRIPEIIGVKSQEASQTLSDSVYSHL 651
 DB 588 DPCDLOPIFDDMLHLPNPEELRVIEEIPQAEKDLRIPEIIGVKSQEASQTLSDSVYSHL 647

QY 652 PDLL 655
 DB 648 PDLL 651

RESULT 3
 Q90Y18
 ID Q90Y18 PRELIMINARY; PRT; 132 AA.
 AC Q90Y18;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Death receptor 6 (Fragment).
 GN DR6.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]


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OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE Leukocyte;
RC TISSUE=Leukocyte;
RA Plagueuvelos O.; Secombes C.J.;
RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ345137; CAC43329.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;

Query Match
Best Local Similarity 8.9%; Score 308; DB 13; Length 285;
Matches 67; Conservative 22; Mismatches 79; Indels 20; Gaps 3;

QY 53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFRHENGIEKCHDCSQP 112
Db 30 TYIWRDDATGDSLTCDLCPAGTYLLKHCTKORKSDCGPCPKSHYTEIWNYYIERQYCNRF 89
QY 113 CPWPMIEKLPCAAALTDRECTPPGFMQSNATCAPHTVCPVGMGVRKKGTTEDVRCKQCA 172
Db 90 CTADIESVPTQLNRCQCKDGFYMTWTHGSCSRHRCPPGEGVISNGTAHTDVKCEPCP 149
QY 173 RGTFSVPSVMKXAYTDCLSQNLVWKPGTKETDNCV 211
Db 150 VGFFSAVSSSRKACQKFSVCPGRTTI--PGNDMNDVYC 186

RESULT 8
Q80YS6 PRELIMINARY; PRT; 474 AA.
AC Q80YS6;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor receptor type II.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Kistar; TISSUE=Spleen;
RA Li Y.; Ji A.; Schafer M.K.;
RT "Expression of TNFR2 in rat dorsal root ganglion."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF498039; AAP33151.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9B8C8D714 CRC64;

Query Match
Best Local Similarity 8.1%; Score 281.5; DB 11; Length 474;
Matches 83; Conservative 39; Mismatches 128; Indels 71; Gaps 11;

QY 65 LTCDKCPAGTYVSEHCTNTSLRVSCSPVGTFRHENGIEKCHDCSQPCPWPMEIKLP 124
Db 53 MCCAKCPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSCSDQVETHNCT 112
QY 125 ALTDRECTCPGMP-----QSNATCAPHTVCPVGMGVRKKGTTEDVRCKQARGTFS 177
Db 113 KQNRVCAACNADSYCALXHLHSGNCQCKMLSCGFGFVARSRTNSGNVCSACAPGTF 172
QY 178 DVPSSVMKXAYTDCLSQNLVWKPGTKETDNCVCTLPFSFSSTSPS--PGTAIFPRPE- 234
Db 173 DTSTSDVCRPHRIC-----SILAIFGNASTDAVCA-----SESPTFSAPVPIVVSQPEP 223
QY 235 ----HMETHVEPSST-YVPKGNMST---ESNSASV----- 262
Db 224 TRSQPMDOBPSPSOTPHIPVSLGSIPIEPSITGSGISLPIGLIVGLTLLGLMLGLANCF 283
QY 263 ----RPKVLSSIQEGTVPDNTSSARGKEDVANKLENLQVWVHQOQPHRHILKLLPSMEA 318
Db 284 ILVQRKKPSCLORETVMVPHLPDDKSDAI-----GLEQQLLTITAPSSSS 329
QY 319 TGGEKSSST--PIKGPGRGHR 337
Db 330 SSLESSASAGDRRAPPGGHPQ 350

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OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00852; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 8.0%; Score 275.5; DB 11; Length 433;
Best Local Similarity 26.1%; Pred. No. 2.2e-14;
Matches 83; Conservative 37; Mismatches 127; Indels 71; Gaps 11;

QY 65 LTCDKCPAGTYVSEHCNTNTSLRVSSCPVGTFTRHENGIEKCHDCSQPCFPMIEKLPKA 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 ALTDRECTCPGMF-----QSNATCAPHTVCPVGVGVRKKGTTEDVRCKQCARGTFS 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 93 KQKRVACNADSYCALKLHSGNCRQCKMLSKCGPFGFVARSRTSNGNVICSACAPGTFS 152
QY 178 DVPSSVMKCKAYTDCLSQNLVVKPKTKETDNCVGLPSSSSPS--PGTAFFRPE- 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 DTTSDVCRPHRIC-----SILAIPGNASTDAVCA-----SESTPRAVPTIYVSOPEP 203
QY 235 ---HMETHEVPSST-VYPKGNST---ESNSSASV----- 262
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 TRSQMDQEPGSPQTFPIVSGSTPIETPSITGIGSLPIGLIVGLATLGLMLGLANCF 263
QY 263 ---RPKVLSSIOEGTVPDNTSSARGKEDVKNKLPNLQVNHQGPVHRLKLLPSMEA 318
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 264 ILVQKKKPSCLQRETIVPHLPDEKSDAV-----GLEQQHLTTAPSSSS 309
QY 319 TGGEKSTPIKPKRGHP 336
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 310 SSLESSAS--AGDRAPP 325
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
Q62327 ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (Fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice."
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;

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RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene."
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR PIR; I48854; I48854.
DR HSSP; P19438; INCF.
DR MGI; MGI:1314883; Tnfrsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00852; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
FT NON_TER 87
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 8.0%; Score 275.5; DB 11; Length 459;
Best Local Similarity 25.0%; Pred. No. 2.4e-14;
Matches 82; Conservative 34; Mismatches 127; Indels 85; Gaps 10;

QY 65 LTCDKCPAGTYVSEHCNTNTSLRVSSCPVGTFTRHENGIEKCHDCSQPCFPMIEKLPKA 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 38 MCCAKCPGQYVKHFCNKTSDTVACDCAEASMTQVQNCFRCLSCSSCSTDQVETRACT 97
QY 125 ALTDRECTCPGMFOSNAT-----CAPHTVCPVGVGVRKKGTTEDVRCKQCARGTFS 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 KQKRVACNADSYCALKLHSGNCRQCKMLSKCGPFGFVARSRTSNGNVICSACAPGTFS 157
QY 178 DVPSSVMKCKAYTDCLSQNLVVKPKTKETDNCVGLPSSSSPS--PGTAFFRPEME 237
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 158 DTTSDVCRPHRIC-----SILAIPGNASTDAVCA-----PESPT 193
QY 238 THEVPSSTVY-----PKGNSTESNSSASVRKVLSSIOEGTVPDNTSSARGKEDVKNKLP 293
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 194 LSAIPRTIYVSOPEPTRSQPLDQEPGSPQTFPIETPSITGIGSLPIGLIVGLATLGLMLGL 247
QY 294 -----NLQVNH-----HQQGPH-----HRHLK 311
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 248 IGLIVGVTSLGLMLGLVNCFLVQKKPSCLQKRDVPHVDPKSDAVGLEQQHLTT 307
QY 312 LLPSMEATGGEKST--PIKPKRGHP 337
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 TAPSSSSSSLESSASAGDRAPPGGHP 335

RESULT 13
Q9PUS0 ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]_TaxID=8038;
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in

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the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.
RL Biol. Reprod. 62:420-426 (2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.8%; Score 269.5; DB 13; Length 302;
Best Local Similarity 32.5%; Pred. No. 5e-14;
Matches 53; Conservative 26; Mismatches 81; Indels 3; Gaps 2;

QY 53 TYRHVDRATGQVLTCDCPCAGTYVSEHCTNTSLRVCSSCPVGTTRHENGIEKCHDCSQP 112
Db 22 TFKNDDRVGLSIVCDRCPPGTIRAPCSAMRKSDCAECFNGAYTEFWNHLKLCRCM- 80

QY 113 CPWPMIEKLPCAAALTDRECTCPGGMF--QSNATCAPHTVCPVGMVGRKKGTTETEDVRCKQ 170
Db 81 CAENQVVKQECSPSNCECKEGYFNKYEACIKHKECPGYGANTGTGPHQDTECVQ 140

QY 171 CAGTFSDVPSSVMKCKAYTCLQNLVVIKPGTKETDNCVT 213
Db 141 CQAGFYSESSAKATCLAQSNCKYVGLRVILKQGDWHNLCLAS 183

RESULT 14
O88734 PRELIMINARY; PRT; 482 AA.
ID O88734
AC O88734
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE P80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
and Characterization of the two Transcripts."
RL Genomics 52:79-98 (1998).
DR EMBL; Y14619; CAA74969.1; -.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; O92956; 1JVA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 7.6%; Score 262.5; DB 11; Length 482;
Best Local Similarity 24.4%; Pred. No. 3.2e-13;
Matches 82; Conservative 33; Mismatches 128; Indels 93; Gaps 11;

QY 65 LTCDCPCAGTYVSEHCTNT-----SLRVCSSCPVGTTRHENGIEKCHDCSQPCPWPM 117
Db 53 MCCACPPQYVVKHFNKTSITVCDADSDTVACDCAASYITQWNQFRTCLSCSSCSSTDO 112
QY 118 IEKLPCAAALTDRECTCPGGMFQSNAT-----CAPHTVCPVGMVGRKKGTTETEDVRCKQ 170
Db 113 VETRACTKQNRVCAACEAGRYCALKTHSGSCRCQMLSKCGPGFGVASSRAPGNVLCKA 172
QY 171 CAGTFSDVPSSVMKCKAYTCLQNLVVIKPGTKETDNCVTLSLPSFSSSTSPSPTAIF 230
Db 173 CAPGTFSDTTSSTDVCRPHRIC-----SILAIFGNASTDAVCA----- 210
QY 231 PRPEHMETHEVPSSTYV-----PKGMNSTESNSASVRPKVLSSIOEGTVPDNTSSARGKE 286
Db 211 --PESPTLSAIRTLVVSQPEPTRSQPLDQEPGQSTPSILTSL--GSPTIIEQSTKG-- 264
QY 287 DVNKTLP-----NLQVNV-----HQQGP----- 305
Db 265 --GISLFIGLIVGTVSLGLMLGLVNCFLVQRKKPSCLORDAKVPHVDPDEKSDAVGL 322
QY 306 -HRHILKLPSEMEATGEXSSTPI---KGPKEGHPR 337
Db 323 EQHLLTAPSSSSSSSSLESSASAGDRRAPPGGHQ 358

RESULT 15
O80010 PRELIMINARY; PRT; 467 AA.
AC O80010
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE CD30 protein precursor.
GN CD30.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Burgess S.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Burgess S.C.;
RL Thesis (1998); Bristol University, U.K.
EMBL; AJ276964; CAC79223.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Signal.
FT SIGNAL.
FT CHAIN CD30 protein.
SQ SEQUENCE 467 AA; 51350 MW; F9AD4F77DEEC9588 CRC64;

Query Match 7.6%; Score 262; DB 13; Length 467;
Best Local Similarity 29.0%; Pred. No. 3.3e-13;
Matches 86; Conservative 36; Mismatches 129; Indels 46; Gaps 12;

QY 11 LASCRIARRATATMIAGSLLILGLFLSTTTA-OPEQKASNLIGTYRH--VDRATGQVLTC 67
Db 1 MASCS-----LRLGLWLLLLQDIQAGPQPTTSHSCDITLKNWYDETGLR--CC 49
QY 68 DKCPAGTYVSEHCTNTSLRVCSSCPVGTTRHENGIEKCHDCSQPC--PWPMEKLPCAA 125
Db 50 YQCPSGYAKKSCPMDEDCNRCGEQYL-NQSPKPCDACVL-CTKEFDLVEKAPCSF 107
QY 126 LTIRECTCPGGMFQSNAT-----CAPHTVCPVGMVGRKKGTTETEDVRCKQCARGFSDV 179

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Db      108 NSSRVCECRPGMFCQTAAKNTCMRCQRHTACKPGFGVKIRGTSETDVSCEECPPGTFSQ 167
Qy      180 PSSVMKCKAYTDLSONLVWIKPGTKETDNVC-GTLPSPSSSTSPSPGTAIFPRPEHMET 238
Db      168 SSTDVCKRPHTDCAKLNKVAQCKGNATHDQVCTDQPSYL-----TPDTSSI-----RIT 217
Qy      239 HEVPSSTYVPKGMNSTESNSASVRPKVLSIQEGTVPDNTSSARGKEDVNKTLPLNL 295
Db      218 NETDSDVILKRAN-----PVTLASILSSATTEIPGSTPEEALAGTSPTL 263

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Search completed: September 21, 2004, 22:44:03
 Job time : 133 secs